## SEQUENCE LISTING

Zho Goo Liu Asu Rer Zha Zha Xue Yar Wel	Tang, Y. 7 Du, Ping Du, Ping Du, Chenghua Indi, Vinod In, Feiyan Ing, Jie Ino, Qing A. Indi, Yonghong Ing, Yonghong Inman, Tom Inanac, Rado					
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Val Phe Pro Val Pro Asp Gln Gly Gly Ser His Thr Gln Thr Pro Pro 560

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185

697

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180

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												cag Gln				930
												caa Gln 290				978
												gcc Ala				1026

295	300	305	
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gaa Glu	att Ile	aca Thr 20	tca Ser	gca Ala	aat Asn	tat Tyr	gct Ala 25	ggt Gly	gtc Val	tgt Cys	aca Thr	tca Ser 30	tct Ser	gtg Val	att Ile	153
aaa Lys	gaa Glu 35	gaa Glu	aac Asn	att Ile	gat Asp	caa Gln 40	cca Pro	gga Gly	tac Tyr	tgt Cys	tat Tyr 45	ctc Leu	tca Ser	cct Pro	gat Asp	201
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aca Thr	gag Glu	aaa Lys	gga Gly	ctg Leu 70	aaa Lys	caa Gln	ttg Leu	ctt Leu	cca Pro 75	ggg Gly	gtt Val	cca Pro	ttc Phe	ctc Leu 80	tgt Cys	297
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Arg	g Met	Lys	Val 245	Lys	Asn	Arg	Leu	Phe 250	Ala	Lys	Ser	Val	Thr 255	Ser	Asp	
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cc <sup>†</sup> Pro	att Ile 275	gcc Ala	atc Ile	tgg Trp	gtg Val	tct Ser 280	tgt Cys	ggt Gly	gaa Glu	cca Pro	ttt Phe 285	cta Leu	cct Pro	cca Pro	aat Asn	921
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ga As	c aga o Arg	att Ile	ttg Leu	gct Ala 310	gat Asp	cta Leu	gat Asp	acc Thr	atg Met 315	aga Arg	cac His	aaa Lys	atg Met	aga Arg 320	cag Gln	1017
tt. Le	a aaa ı Lys	ggg Gly	cgg Arg 325	cga Arg	gta Val	gcg Ala	gca Ala	tgt Cys 330	cag Gln	cca Pro	gcc Ala	acc Thr	atg Met 335	gtt Val	cct Pro	1065
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gc Al 37	a cac a His O	ctt Leu	tct Ser	gaa Glu	atc Ile 375	caa Gln	gaa Glu	atg Met	gaa Glu	tcc Ser 380	aaa Lys	ata Ile	aat Asn	ttt Phe	cca Pro 385	1209
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cc Pr	c aac o Asn	aca Thr	aaa Lys 405	cga Arg	gtg Val	tgg Trp	att Ile	tat Tyr 410	cta Leu	aat Asn	gga Gly	ggc Gly	aga Arg 415	cct Pro	gaa Glu	1305
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tg Cy	c tcc s Ser 435	Ser	cgt Arg	ctc Leu	aaa Lys	atg Met 440	acc Thr	cac His	cca Pro	gct Ala	aga Arg 445	gca Ala	ctg Leu	tac Tyr	acc Thr	1401
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470 475 480

4/0 4/5 480	
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cag ggc cct caa gcc aca gac att gtg gtg tca cca tcc acg aag ctg Gln Gly Pro Gln Ala Thr Asp Ile Val Val Ser Pro Ser Thr Lys Leu 500 505 510	
ctg tct ctg gca cat ctc cac aat taa ctcct atcagaacca tcggattttc Leu Ser Leu Ala His Leu His Asn * 515 520	1645
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ctaacagact gctctgggca tcttttctct ttgccttggc caggcctctc agaattga	gt 1945
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ggc tgt aat aca aaa gct gcg cgt ccc tta att tcc tcg gcg gtt tat Gly Cys Asn Thr Lys Ala Ala Arg Pro Leu Ile Ser Ser Ala Val Tyr 25 30 35	149

gtg aag aac cag ctc agt ggg act cta cag att aaa cca ggg gtt ttc Val Lys Asn Gln Leu Ser Gly Thr Leu Gln Ile Lys Pro Gly Val Phe

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tgt Cys 70	ttg Leu	aac Asn	aga Arg	ata Ile	aag Lys 75	agt Ser	ttc Phe	agg Arg	tac Tyr	cct Pro 80	tgg Trp	gcg Ala	aga Arg	ctg Leu	tac Tyr 85	293
agt Ser	act Thr	tcc Ser	caa Gln	acc Thr 90	act Thr	gtc Val	gac Asp	agc Ser	ggt Gly 95	gag Glu	gta Val	aaa Lys	acc Thr	ttc Phe 100	ttg Leu	341
gcc Ala	ctg Leu	gct Ala	cac His 105	aaa Lys	tgg Trp	tgg Trp	gat Asp	gaa Glu 110	caa Gln	gga Gly	gta Val	tat Tyr	gca Ala 115	cct Pro	ctt Leu	389
cat His	tcc Ser	atg Met 120	aat Asn	gac Asp	ctg Leu	agg Arg	gtg Val 125	cca Pro	ttt Phe	att Ile	agg Arg	gac Asp 130	aat Asn	ctt Leu	ctg Leu	437
aaa Lys	aca Thr 135	att Ile	cct Pro	aat Asn	cac His	cag Gln 140	cca Pro	gga Gly	aaa Lys	cct Pro	ttg Leu 145	ttg Leu	ggg Gly	atg Met	aag Lys	485
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cgg Arg	ctt Leu	Gly	gct Ala	tca Ser 170	gtt Val	att Ile	gga Gly	atc Ile	gaç Asp 175	cct Pro	gtg Val	gat Asp	gag Glu	aac Asn 180	att Ile	581
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ata Ile	gag Glu	tac Tyr 200	aga Arg	gtg Val	tgt Cys	tcc Ser	ctg Leu 205	gaa Glu	gag Glu	att Ile	gtg Val	gaa Glu 210	gag Glu	act Thr	gca Ala	677
gaa Glu	aca Thr 215	ttt Phe	gat Asp	gct Ala	gtt Val	gta Val 220	gct Ala	tct Ser	gaa Glu	gtt Val	gta Val 225	gaa Glu	cat His	gtg Val	att Ile	725
					tta Leu 235											773
ggt Gly	tct Ser	tta Leu	ttc Phe	att Ile 250	act Thr	aca Thr	atc Ile	aac Asn	aaa Lys 255	aca Thr	caa Gln	ctt Leu	tcc Ser	tat Tyr 260	gcc Ala	821
ttg Leu	gga Gly	att Ile	gtt Val 265	ttt Phe	tca Ser	gag Glu	caa Gln	att Ile 270	gca Ala	ggt Gly	att Ile	gta Val	cca Pro 275	aaa Lys	ggt Gly	869
act	cat	aca	tgg	gag	aag	ttt	gtt	tca	cct	gaa	aca	cta	gag	agc	att	917

Thr His Thr Trp Glu Lys Phe Val Ser Pro Glu Thr Leu Glu Ser Ile 280 285 290	
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aac ccc ttc tca ggt tac tgg cat tgg agt gaa aat acc agc ctt aac Asn Pro Phe Ser Gly Tyr Trp His Trp Ser Glu Asn Thr Ser Leu Asn 310 315 320 325	1013
tat gca gct cat gct gtg aaa tcc agg gtc cag gaa cac cca gcc tct Tyr Ala Ala His Ala Val Lys Ser Arg Val Gln Glu His Pro Ala Ser 330 335 340	1061
gct gag ttt gtt tta aag gga gaa aca gaa gag ctc caa gct aat gcc Ala Glu Phe Val Leu Lys Gly Glu Thr Glu Glu Leu Gln Ala Asn Ala 345 350 355	1109
tgc acc aat cca gct gtg cat gaa aag ctg aag aaa tga attgtttctg Cys Thr Asn Pro Ala Val His Glu Lys Leu Lys Lys * 360 365 370	1158
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_	_				ccc Pro			_	-		_		_			368
_					tat Tyr	_	_	_	_			-	_		_	416
		-	-		aag Lys	_	_		_			-				464
_		_	_	_	cac His 105	_	_					_		_		512
_	~				ctg Leu	_			_	_		_		-		560
					ttt Phe											608
-					tct Ser	_	_					-			-	656
	_			_	gat Asp		_		_	-						704
					cca Pro 185											752
					gca Ala											800
					atg Met											848
					agt Ser											896
					tct Ser											944

245 250 255

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gaa Glu	aca Thr	gac Asp	ctt Leu 295	ccc Pro	cag Gln	ata Ile	cga Arg	tcg Ser 300	acc Thr	tta Leu	att Ile	ccc Pro	att Ile 305	tta Leu	cat His	108	8
caa Gln	aaa Lys	gca Ala 310	aag Lys	agg Arg	ggt Gly	act Thr	cca Pro 315	cac His	caa Gln	gca Ala	aaa Lys	cag Gln 320	gct Ala	gtg Val	cac His	113	6
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		aag Lys	_			_	_	-					_	_	1904
	_	tat Tyr	_	_			_		_		_		_		1952
		aca Thr													2000
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		gaa Glu	_												2288

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gca	ggct	cca	gctt	ctgc	aa a	aact	tgga	t tc	acaa	atgt	ccc	tgaa	cag	aaaa	tgaagc	3027

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					aag Lys 20											396
					gtt Val											444
					gac Asp											492
					agc Ser											540
					att Ile											588
					ttt Phe 100											636
					att Ile											684
					cgg Arg											732
					tgc Cys											780
					ttc Phe											828
					ggg Gly 180											876
					gtc Val											924
					tac Tyr											972
					ccg Pro											1020
acc	aac	agt	gcc	cgg	gaa	agg	aag	atc	aac	tca	tcc	ctg	cag	ctc	cca	1068

Thr	Asn 240	Ser	Ala	Arg	Glu	Arg 245	Lys	Ile	Asn	Ser	Ser 250	Leu	Gln	Leu	Pro	
		gtg Val														1116
		agc Ser														1164
		gta Val														1212
		ggc Gly 305														1260
		gtg Val														1308
		cag Gln														1356
gcc Ala	tca Ser	cac His	tcg Ser	ggc Gly 355	gta Val	gtc Val	cag Gln	gtg Val	ccc Pro 360	atg Met	gcc Ala	aac Asn	tgc Cys	agc Ser 365	ctg Leu	1404
tac Tyr	agg Arg	agc Ser	tgt Cys 370	ggg Gly	gac Asp	tgc Cys	ctc Leu	ctc Leu 375	gcc Ala	cgg Arg	gac Asp	ccc Pro	tac Tyr 380	tgt Cys	gct Ala	1452
tgg Trp	agc Ser	ggc Gly 385	tcc Ser	agc Ser	tgc Cys	aag Lys	cac His 390	gtc Val	agc Ser	ctc Leu	tac Tyr	cag Gln 395	cct Pro	cag Gln	ctg Leu	1500
gcc Ala	acc Thr 400	agg Arg	ccg Pro	tgg Trp	atc Ile	cag Gln 405	gac Asp	atc Ile	gag Glu	gga Gly	gcc Ala 410	agc Ser	gcc Ala	aag Lys	gac Asp	1548
ctt Leu 415	tgc Cys	agc Ser	gcg Ala	tct Ser	tcg Ser 420	gtt Val	gtg Val	tcc Ser	ccg Pro	tct Ser 425	ttt Phe	gta Val	cca Pro	aca Thr	ggg Gly 430	1596
gag Glu	aag Lys	cca Pro	tgt Cys	gag Glu 435	caa Gln	gtc Val	cag Gln	ttc Phe	cag Gln 440	ccc Pro	aac Asn	aca Thr	gtg Val	aac Asn 445	act Thr	1644
		tgc Cys														1692
aac Asn	ggg Gly	gcc Ala	ccc Pro	gtc Val	aat Asn	gcc Ala	tcg Ser	gcc Ala	tcc Ser	tgc Cys	cac His	gtg Val	cta Leu	ccc Pro	act Thr	1740

475 470 465 1788 ggg gac ctg ctg ctg gtg ggc acc caa cag ctg ggg gag ttc cag tgc Gly Asp Leu Leu Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys 490 485 480 1836 tgg tca cta gag gag ggc ttc cag cag ctg gta gcc agc tac tgc cca Trp Ser Leu Glu Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro 500 495 1884 gag gtg gtg gag gac ggg gtg gca gac caa aca gat gag ggt ggc agt Glu Val Val Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser 520 515 1932 gta ccc gtc att atc agc aca tcg cgt gtg agt gca cca gct ggt ggc Val Pro Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly 535 530 aag gcc agc tgg ggt gca gac agg tcc tac tgg aag gag ttc ctg gtg 1980 Lys Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val 545 atg tgc acg ctc ttt gtg ctg gcc gtg ctg ctc cca gtt tta ttc ttg 2028 Met Cys Thr Leu Phe Val Leu Ala Val Leu Pro Val Leu Phe Leu 560 565 2076 ctc tac cgg cac cgg aac agc atg aaa gtc ttc ctg aag cag ggg gaa Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln Gly Glu 580 tgt gcc agc gtg cac ccc aag acc tgc cct gtg gtg ctg ccc cct gag 2124 Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu Pro Pro Glu 595 acc cgc cca ctc aac ggc cta ggg ccc cct agc acc ccg ctc gat cac 2172 Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr Pro Leu Asp His 615 610 cga ggg tac cag tcc ctg tca gac agc ccc ccg ggg gcc cga gtc ttc 2220 Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro Gly Ala Arg Val Phe 630 625 act gag tca gag aag agg cca ctc agc atc caa gac agc ttc gtg gag 2268 Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile Gln Asp Ser Phe Val Glu 645 640 gta tcc cca gtg tgc ccc cgg ccc cgg gtc cgc ctt ggc tcg gag atc 2316 Val Ser Pro Val Cys Pro Arg Pro Arg Val Arg Leu Gly Ser Glu Ile 665 670 660 655 cgt gac tct gtg gtg tga gagctg acttccagag gacgctgccc tggcttcagg 2370 Arg Asp Ser Val Val 675 2430 ggctgtgaat gctcggagag ggtcaactgg acctcccctc cgctctgctc ttcgtggaac

2490

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Gln Val Ala Glu Ser Asp Leu Ser Asp Asp Gly Lys Ala Ser Leu Val

25

30

35

agc gag gaa gag gaa gat gaa gaa gat aag gct acc cct aga aga 199

Ser	Glu	Glu	Glu 40	Glu	Asp	Glu	Glu	Glu 45	Asp	Lys	Ala	Thr	Pro 50	Arg	Arg	
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					gcc Ala											295
cag Gln 85	ttg Leu	ttt Phe	tct Ser	agc Ser	gca Ala 90	cgc Arg	tta Leu	cag Gln	aat Asn	gag Glu 95	aaa Lys	aaa Lys	aca Thr	att Ile	ctt Leu 100	343
					tgt Cys											391
					gac Asp											439
					acc Thr											487
					gaa Glu											535
					gct Ala 170											583
					acg Thr											631
cct Pro	cct Pro	gag Glu	aag Lys 200	ttt Phe	gct Ala	cta Leu	gag Glu	aac Asn 205	ttc Phe	act Thr	gtc Val	tca Ser	gcc Ala 210	gct Ala	aaa Lys	679
					tac Tyr											727
					aga Arg											775
					gaa Glu 250											823
					gat Asp											871

	265	270		275	
cga caa aag acc Arg Gln Lys Thr 280				n Gly Cys	19
tgt ggt gtg cga Cys Gly Val Arg 295	Gly Gln Phe C			~	67
ggg gag gat gtc Gly Glu Asp Val 310					15
ccc tgt cgt ggg Pro Cys Arg Gly 325					63
cgc tgt gcc aca Arg Cys Ala Thr					.11
gac aat gtt aag Asp Asn Val Lys 360				u Val Glu	.59
gac aat taa gagg Asp Asn * 375	gaaa acaaacaga	a ccagccaco	t caccatagag t	actccaaca 12	15
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tcctacctct tgagt	actgg gattaca	gtc gtgtccc	aca cgctcagccc	tgagttagtt 20	55

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gcc ggc ccc att cca gaa gca gag acc agg gga gcc aag aga att tcc

Ala	Gly	Pro	Ile 40	Pro	Glu	Ala	Glu	Thr 45	Arg	Gly	Ala	Lys	Arg 50	Ile	Ser	
													aac Asn			605
													ggc Gly			653
													agt Ser			701
													tct Ser			749
													acc Thr 130			797
													gac Asp			845
													gcc Ala			893
													gag Glu			941
													cgg Arg			989
													acc Thr 210			1037
cgg Arg	gcc Ala	tca Ser 215	gag Glu	agc Ser	agc Ser	gcc Ala	tct Ser 220	tcc Ser	gac Asp	ggc Gly	ctc Leu	cat His 225	cca Pro	gtc Val	atc Ile	1085
acc Thr	ccg Pro 230	tca Ser	cgg Arg	gcc Ala	tca Ser	gag Glu 235	agc Ser	agc Ser	gcc Ala	tct Ser	tcc Ser 240	gac Asp	ggc Gly	ccc Pro	cat His	1133
													act Thr			1181
gct Ala	gaa Glu	gcc Ala	ctg Leu	gtg Val	act Thr	gtc Val	aca Thr	aac Asn	atc Ile	gag Glu	gtt Val	att Ile	aat Asn	tgc Cys	agc Ser	1229

265 270 275 1277 atc aca gaa ata gaa aca acg act tcc agc atc cct ggg gcc tca gac Ile Thr Glu Ile Glu Thr Thr Thr Ser Ser Ile Pro Gly Ala Ser Asp 280 285 1325 aca gat ctc atc ccc acg gaa ggg gtg aag gcc tcg tcc acc tcc gat Thr Asp Leu Ile Pro Thr Glu Gly Val Lys Ala Ser Ser Thr Ser Asp 295 300 cca cca gct ctg cct gac tcc act gaa gca aaa cca cac atc act gag 1373 Pro Pro Ala Leu Pro Asp Ser Thr Glu Ala Lys Pro His Ile Thr Glu 310 315 gtc aca gcc tct gcc gag acc ctg tcc aca gcc ggc acc aca gag tca 1421 Val Thr Ala Ser Ala Glu Thr Leu Ser Thr Ala Gly Thr Thr Glu Ser 325 330 gct gca cct cat gcc acg gtt ggg acc cca ctc ccc act aac agc gcc 1469 Ala Ala Pro His Ala Thr Val Gly Thr Pro Leu Pro Thr Asn Ser Ala 345 350 aca gaa aga gaa gtg aca gca ccc ggg gcc acg acc ctc agt gga gct 1517 Thr Glu Arg Glu Val Thr Ala Pro Gly Ala Thr Thr Leu Ser Gly Ala 360 ctg gtc aca gtt agc agg aat ccc ctg gaa gaa acc tca gcc ctc tct 1565 Leu Val Thr Val Ser Arg Asn Pro Leu Glu Glu Thr Ser Ala Leu Ser 380 gtt gag aca cca agt tac gtc aaa gtc tca gga gca gct ccg gtc tcc 1613 Val Glu Thr Pro Ser Tyr Val Lys Val Ser Gly Ala Ala Pro Val Ser 395 ata gag gct ggg tca gca gtg ggc aaa aca act tcc ttt gct ggg agc 1661 Ile Glu Ala Gly Ser Ala Val Gly Lys Thr Thr Ser Phe Ala Gly Ser 405 410 415 1709 tet get tee tee tae age eee teg gaa gee gee ete aag aac tte ace Ser Ala Ser Ser Tyr Ser Pro Ser Glu Ala Ala Leu Lys Asn Phe Thr 425 430 cct tca gag aca ccg acc atg gac atc gca acc aag ggg ccc ttc ccc 1757 Pro Ser Glu Thr Pro Thr Met Asp Ile Ala Thr Lys Gly Pro Phe Pro 440 445 acc agc agg gac cct ctt cct tct gtc cct ccg act aca acc aac agc 1805 Thr Ser Arg Asp Pro Leu Pro Ser Val Pro Pro Thr Thr Asn Ser 455 460 agc cga ggg acg aac agc acc tta gcc aag atc aca acc tca gcg aag 1853 Ser Arg Gly Thr Asn Ser Thr Leu Ala Lys Ile Thr Thr Ser Ala Lys 470 475 acc acg atg aag ccc cca aca gcc acg ccc acg act gcc cgg acg agg 1901 Thr Thr Met Lys Pro Pro Thr Ala Thr Pro Thr Thr Ala Arg Thr Arg 485 490 495 500

ccg acc aca gac gtg agt gca ggt gaa aat gga ggt ttc ctc ctg Pro Thr Thr Asp Val Ser Ala Gly Glu Asn Gly Gly Phe Leu Leu 505 510 515	1949
cgg ctg agt gtg gct tcc ccg gaa gac ctc act gac ccc aga gtg gca Arg Leu Ser Val Ala Ser Pro Glu Asp Leu Thr Asp Pro Arg Val Ala 520 525 530	1997
gaa agg ctg atg cag cag ctc cac cgg gaa ctc cac gcc cac gcg cct Glu Arg Leu Met Gln Gln Leu His Arg Glu Leu His Ala His Ala Pro 535 540 545	2045
cac ttc cag gtc tcc tta ctg cgt gtc agg aga ggc taa cggacatcag His Phe Gln Val Ser Leu Leu Arg Val Arg Arg Gly * 550 555 560	2094
ctgcagccag gcatgtcccg tatgccaaaa gagggtgctg cccctagcct gggcccccac	2154
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taaccaacac aggccccagc acccgcagag cagacactgc g atg aca acg gac Met Thr Thr Asp	413

gac aca gaa gtg ccc gct atg act cta gca ccg ggc cac gcc gct ctg 461

Asp 5	Thr	Glu	Val	Pro	Ala 10	Met	Thr	Leu	Ala	Pro 15	Gly	His	Ala	Ala	Leu 20	
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					gaa Glu											557
					agg Arg											605
					tcc Ser											653
					acc Thr 90											701
					gac Asp											749
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					tcc Ser											845
					ccc Pro											893
					gtg Val 170											941
					gaa Glu											989
					ccc Pro											1037
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					gcc Ala											1133

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405	PIO	THE	THE	ASP	410	ser	Ala	GIÀ	GIU	415	GīĀ	GIÀ	rne	ъеи	420	
_		_	_	gtg Val 425	_		_	_	_			_		_	-	1709
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65

606

636

70

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agc cgc cgg gag atc gag gag ctg cta gca gaa gcc aag tac tac cta Ser Arg Arg Glu Ile Glu Glu Leu Leu Ala Glu Ala Lys Tyr Tyr Leu

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act to Thr T																781
gaa ca Glu G																829
tac aa Tyr A																877
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aac g Asn G 205																973
tgc to Cys Ti																1021
acc to Thr So																1069
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ggg ge Gly A 285																1213
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1435

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Tyr Asp Ile Cys Asp Glu Asp Cys His Gly Ser Cys Ser Asp Thr Ser

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Phe											tgc Cys		871
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			tgc Cys 20												gtg Val		213
			aag Lys														261
			ggc Gly														309
			gtg Val														357
			ggc Gly														405
			gct Ala 100														453
			gat Asp													!	501
			aac Asn													į	549
			aag Lys													į	597

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<sup>&</sup>lt;211> 2099

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cac acg gtg aag ggg aca ccc ttt gag acc ccg gac cag ggc aag gcg His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala 65 70 75 80	358
agg ctg cta acc cac tgg gag cag atg gat tat ggg gtc cag ttc acg Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Val Gln Phe Thr 85 90 95	406
gcc tct cgg aag ttc ttg acc atc aca ccc atc gtg ctg tac ttc ctc Ala Ser Arg Lys Phe Leu Thr Ile Thr Pro Ile Val Leu Tyr Phe Leu 100 105 110	454
acc agc ttc tac act aag tac gac cag atc cat ttt gtg ctc aac acc Thr Ser Phe Tyr Thr Lys Tyr Asp Gln Ile His Phe Val Leu Asn Thr 115 120 125	502
gtg tcc ctg atg agc gtg ctt atc ccc aag ctg ccc cag ctc cac gga Val Ser Leu Met Ser Val Leu Ile Pro Lys Leu Pro Gln Leu His Gly 130 135 140	550
gtc cgg att ttt gga atc aat aag tac tga g agtgcagccc cttcccctgc Val Arg Ile Phe Gly Ile Asn Lys Tyr * 145	601
ccagggtggc aggggagggg tagggtaaaa ggcatgtgct gcaacactga agacagaaag	661
aagaagcctc tggacactgc cagagatggg ggttgagcct ctggcctaat ttccccctc	721
gcttccccca gtagccaact tggagtagct tgtagtgggg ttggggtagg ccccctgggc	781
tctgaccttt tctgaatttt ttgatctttt ccttttgctt tttgaataga gactccatgg	841
agttggtcat ggaatgggct gggctcctgg gctgaacatg gaccacgcag ttgcgacagg	901
aggccagggg aaaaacccct gctcacttgt ttgccctcag gcagccaaag cactttaacc	961
cctgcatagg gagcagaggg cggtacggct tctggattgt ttcactgtga ttcctaggtt	1021

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gctggtaact ttggcgcctc cgccaagccc tgccagactc ccctggctgt gatggcattc 180
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<sup>&</sup>lt;211> 1605

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (535)..(1050)

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1128

accocaggig cictiticat ggiggigcci gcicatctig cigatgcaaa ciaggaagit

aggctgcatc tcggagtggc tttcgctgga gaggtgcttt gctgtctctc agactcagtc 1188 actgtgttcc ctccccgcct ctcttatctc catggctgtt tgcagctctc ccaggtactt 1248 tggggtctga gctggaattc ctttgtggtt tgctcttctg cttctcactc ttgtattaag 1308 aaggattcca caaagggaga gtggcatccc tgctgctgct gtgccagacc agagtttcct 1368 gaggggccct gaccctaacc ctccagctca gccctgtaca cctgaccctg taaatgagtg 1428 gggtttgctg actgtaatcc ctgacaccag taaaaccaaa aggactcttg ggggctcagt 1488 gtgagagcca gggttaccta ctctgccaag tgaggacaaa ctgctaggct gtatcccata 1548 atttcaggat gagaaacatt aacaataaaa atttgtagta aacataaaaa aaaaaaa 1605

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<222> (210)..(1172)

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Gly Gly Pro Gly Gly Pro Gly Met Gly Asn Arg Gly Gly
10 15 20

ttc cgc gga ggt ttc ggc agt ggc atc cgg ggc cgg ggt cgc ggc cgt
Phe Arg Gly Gly Phe Gly Ser Gly Ile Arg Gly Arg Gly Arg Gly Arg
25 30 35 40

gga cgg ggc cgg ggc cgc gga gct cgc gga gct cgc gga ggc aag gcc gag

Gly Arg Gly Arg Gly Arg Gly Ala Arg Gly Gly Lys Ala Glu

45

50

55

gat aag gag tgg atg ccc gtc acc aag ttg ggc cgc ttg gtc aag gac 425
Asp Lys Glu Trp Met Pro Val Thr Lys Leu Gly Arg Leu Val Lys Asp
60 65 70

atg aag atc aag tcc ctg gag gag atc tat ctc ttc tcc ctg ccc att 473

Met	Lys	Ile 75	Lys	Ser	Leu	Glu	Glu 80	Ile	Tyr	Leu	Phe	Ser 85	Leu	Pro	Ile	
		Ser						ttc Phe								521
								cag Gln								569
_				_	-		-	gct Ala			_					617
								aag Lys 145								665
	_			-	-	_		tcc Ser		_			_	_		713
				-			_	ccc Pro			-		_	-		761
								caa Gln	-			-		_		809
_			_		_		-	cgg Arg		_			-			857
								gat Asp 225								905
								ggc Gly								953
								ctt Leu								1001
								tgc Cys								1049
								cat His								1097
								gaa Glu								1145

tcc tta ata ggc agg gag aag aga tag atcac cactccaggg acttagatct Ser Leu Ile Gly Arg Glu Lys Arg * 315 320	1197
tcatgtcctt ggaccaagcg gccacaactt cggtgacggg gcatccactc cttatcgctc	1257
ggccttgcgc tccagcgagc tccgcaggca catcggccca caggccacac agtcacacag	1317
gccgcagacc accaggccac cagagtgcac agcatgcaca gaaacactgc cgcaggaagc	1377
acacacagcg gcttcccaca tcacaagggc cacaatgggc ccccagggcc caccccgctg	1437
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	60
gccgctatta ccactgaacc cggaccccct acccaggtcc agggccagcc gcc atg Met 1	60 116
Met	
Met  1  acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt  Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe	116
acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe  5 10 15  gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp	116
acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe 5 10 15  gtt tgc acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp 20 25 30  ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala	116 164 212
acg aac gtg tac tcc ttg gat ggg att ctg gtg ttt ggt ttg ctc ttt Thr Asn Val Tyr Ser Leu Asp Gly Ile Leu Val Phe Gly Leu Leu Phe  10 ctg acc tgt gcc tac ttc aag aaa gta cct cgt ctc aaa acc tgg Val Cys Thr Cys Ala Tyr Phe Lys Lys Val Pro Arg Leu Lys Thr Trp  20 ctg cta tca gag aag aag ggt gtt tgg ggt gtg ttt tac aaa gcc gct Leu Leu Ser Glu Lys Lys Gly Val Trp Gly Val Phe Tyr Lys Ala Ala  35 40 45  gtg att gga acc agg ctg cat gct gtg gca att gct tgt gta Val Ile Gly Thr Arg Leu His Ala Ala Val Ala Ile Ala Cys Val Val	116 164 212 260

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55

70

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His Gly Lys Phe His Gly Thr Val Lys Ala Glu Asn Gly Lys Leu Val

atc aat gga aat ccc atc acc atc ttc cag gag cga gat ccc tcc aaa

Ile Asn Gly Asn Pro Ile Thr Ile Phe Gln Glu Arg Asp Pro Ser Lys

75

80

atc Ile 85	Lys	tgg Trp	ggc	gat Asp	gct Ala 90	Gly	gct Ala	gag Glu	tac Tyr	gtc Val 95	Val	gag Glu	tcc Ser	act Thr	ggc Gly 100	4	102
												cag Gln				4	150
												ccc Pro				4	198
												aag Lys 145				5	46
												gcc Ala				5	94
												aca Thr				6	42
atc Ile	act Thr	gcc Ala	acc Thr	cag Gln 185	aag Lys	act Thr	gtg Val	gga Gly	tgg Trp 190	ccc Pro	ctt Leu	ccg Pro	gga Gly	aac Asn 195	tgt Cys	6	90
												atc Ile				7	38
												gag Glu 225				7	86
												aac Asn				8	34
												tat Tyr				88	82
												aag Lys				93	30
		Thr										aac Asn				97	78
cac His	Ser	tcc Ser 295	acc Thr	ttt Phe	gac Asp	Ala	300 ggg	gct Ala	ggc Gly	att Ile	gcc Ala	ctc Leu 305	aac Asn	gac Asp	cac His	102	26
ttt	gtc	aag	ctc	att	tcc	tgg	tat	gac	aac	gaa	ttt	ggc	tac	agc	aac	107	74

Phe Val Ly 310	vs Leu Ile Ser Trp Tyr 315	Asp Asn Glu	Phe Gly Tyr Ser Asn 320	
agg gtg gt Arg Val Va 325	ng gac ctc atg gcc cac al Asp Leu Met Ala His 330	atg gcc tcc Met Ala Ser 335	Lys Glu *	1123
ggaccaccag	ccccagcaag agcacaaga	g gaagagagag	acceteactg etggggagte	1183
cctgccacac	teagteece accacactg	a atctcccctc	ctcacagttg ccatgtagac	1243
cccttgaaga	ggggaggggc ctagggagc	c gcaccttgtc	atgtaccatc aataaagtac	1303
cctgtgctca	accaaaaaa aaaaaa	·		1329
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	· <del>-</del>	gctggagaaa	caaaccagac gcagctgaag	60
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gacagttctg	ggtgtagagg actcacatco	: cagagaggct	gaggaagggt ttaccaccgc	240
aagctttctc	aggcgggctc ttgaggggtg	gctggggtct	tcctggcgac gggcctgcgg	300
cactggaagc	cctactggag tttggcctgt	ctccggcaca	ggtttggacg gagctgtttt	360
gtgctgaaag	gttttctcgg ggtccgtggt	gtcccccaaa	ggtgccaccg tgcgggtctc	420
ctagctccct	gccagcttcc tgtccctgtg	ctcactgccc	ccacgcctcc tgccaaggcc	480
gagccacaca	cccgctccac ctgcatttcc	tctaccgact	cgccagccca a atg ccg Met Pro 1	537
ctc ttc act Leu Phe Thr	c ctg gcc tcg ctg agc Leu Ala Ser Leu Ser 10	ggc tgc ccg Gly Cys Pro	agg agg agc tct agg Arg Arg Ser Ser Arg 15	585
ccg acg ccc Pro Thr Pro 20	c acc gca ggc ctt aca o Thr Ala Gly Leu Thr 25	gtc ttc tct Val Phe Ser	gga cgc tcc ctt gca Gly Arg Ser Leu Ala 30	633

gat gca ccg tgg cct ggc ggc gag ccc ccg gtc acc ttc ctc cgc acg 681

Asp 35	Ala	Pro	Trp	Pro	Gly 40	Gly	Glu	Pro	Pro	Val 45	Thr	Phe	Leu	Arg	Thr 50	
							ttc Phe									729
_	_			-	-		ctc Leu	-	_	_	_	_	-			777
-	_		-		_	_	tac Tyr 90		_			-	_		_	825
							tgg Trp		-							873
							gtg Val									921
ctc Leu	-	taa *	agco	cgg	gcac	ccgc	ccc a	igccg	ggct	g gg	gacat	ccct	gad	cacao	tag	977
cttc	ccaç	igg c	tgcc	cccc	ga ca	ıggct	ggct	cto	agto	ggag	gcca	igaga	atc t	ggaa	tcggg	1037
gtca	ıgcgg	igg c	taca	gtco	t to	cago	ggct	cto	ıgggo	cagc	tccc	agco	ctc t	tccc	atgct	1097
ggtg	gcca	icc g	rtgto	cctt	g ct	gcgg	gctgc	ato	ttcc	agt	ctct	ccto	cg t	cttc	cagtg	1157
gccg	ctct	ct t	tata	agaa	ic co	tggt	catt	gaa	ıttta	agg	ссса	cccc	caa g	gtcca	ıgaatg	1217
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<220>

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<222> (291)..(1442)

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gaggaataaa gaagtcacct ccccagctgt catcatcttc cagcagattg agcaagaata 180
ttttgagcac tacaggaaag acagtccatc aaacccgaga tgatgatcag ccacgtgatt 240

ttttcaa	ıgaa	gagg	aata	gg g	tgaa	tgaa	t ct	catc	agaa	aag	cagc	aat	Me	g aat t Asn 1	296
gct ggc Ala Gly															344
aaa agg Lys Arg 20	Gln	_				_			_			~	•	~	392
agc agc Ser Ser 35			-	-		_			-	-				_	440
agc att Ser Ile															488
tgt cag Cys Gln		_					_			_		_		_	536
aaa att Lys Ile															584
gat tcg Asp Ser 100	-	-												•	632
ctc aat Leu Asn 115		-	_	_	_		-		_			_			680
cct ggt Pro Gly							-								728
cca tcc Pro Ser			_			-		_	_	_	-	-		-	776
aac gca Asn Ala				_	_	-			_						824
ggg aag Gly Lys 180															872
act gta Thr Val 195	_	_	_		_	_				-					920

gcc cct ggg acc tca ggg gca ctg aaa agc cct ggg a Ala Pro Gly Thr Ser Gly Ala Leu Lys Ser Pro Gly A 215 220	
att gct agt gct ctg tcc aag cca cta cct cac cag g Ile Ala Ser Ala Leu Ser Lys Pro Leu Pro His Gln G 230 235	
aag tca ggc cct tcc cga aag aaa gct ttt cac cat g Lys Ser Gly Pro Ser Arg Lys Lys Ala Phe His His G 245 250 2	3
cca tca cat tat gca ttt gag act tcc cct aga ccc a Pro Ser His Tyr Ala Phe Glu Thr Ser Pro Arg Pro I 260 265 270	
ggt ggt acc agg ttt tgt tct cag agg caa acc ctt g Gly Gly Thr Arg Phe Cys Ser Gln Arg Gln Thr Leu G 275 280 285	
gaa gaa aaa aaa aaa tca agt aag agt acg aag c Glu Glu Lys Lys Lys Ser Ser Lys Ser Thr Lys Lo 295 300	
gat ctg tcc ggc agt gga agc agc tct aag gtg gaa ac Asp Leu Ser Gly Ser Gly Ser Ser Ser Lys Val Glu Tl 310 315	
att cga gtt ccc aaa cag gca gct gtg att ctg gac to Ile Arg Val Pro Lys Gln Ala Ala Val Ile Leu Asp So 325 330 33	
tgt aag gcc tcc aaa aca caa gca cat gca cat cct ag Cys Lys Ala Ser Lys Thr Gln Ala His Ala His Pro An 340 345 350	
aag gca gag agc tgt ggt cat gcc act gta tcg agt ga Lys Ala Glu Ser Cys Gly His Ala Thr Val Ser Ser Gl 355 360 365	
aaa aca aac gga gta aag caa aac aca tat aaa cta aa Lys Thr Asn Gly Val Lys Gln Asn Thr Tyr Lys Leu Ly 375 380	
aaatgctgaa ttgccaagac ctgcaggtac ctcaatgtta gagcgc	cttcc aaaagtcaaa 1509
atactgtgaa ttttaaggaa ttttacaaat actgacattt aagtaa	aaaaa aaaaaaa 1566

<220>

<sup>&</sup>lt;210> 24

<sup>&</sup>lt;211> 2851

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

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Gly Trp Leu Asp Val Val Gln Ser Leu Ile Arg Val Ile Pro Leu Glu

150 145 140 gat cca ctg gga cca gct gtt ata aca ttg tta cta gat gaa tgt cca 1133 Asp Pro Leu Gly Pro Ala Val Ile Thr Leu Leu Leu Asp Glu Cys Pro 160 155 ttg ccc act aaa gat gca ctc cag aaa ttg act gaa att ctc aat tta 1181 Leu Pro Thr Lys Asp Ala Leu Gln Lys Leu Thr Glu Ile Leu Asn Leu 175 170 1229 aat gga gaa gta gct tgc cag gac tca agc cat cct gcc aaa cac agg Asn Gly Glu Val Ala Cys Gln Asp Ser Ser His Pro Ala Lys His Arg 190 185 1277 aac aca tct gca gtc cta ggc tgc ttg gcc gag aaa cta gca ggt cct Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu Lys Leu Ala Gly Pro 215 205 gca agt ata ggt tta ctt agc cca gga ata ctg gaa tac ttg cta cag 1325 Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu Glu Tyr Leu Leu Gln 220 225 tgt ctg aag tta cag tcc cac ccc aca gtc atg ctt ttt gca ctt atc 1373 Cys Leu Lys Leu Gln Ser His Pro Thr Val Met Leu Phe Ala Leu Ile 240 gca ctg gaa aag ttt gca cag aca agt gaa aat aaa ttg act att tct 1421 Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn Lys Leu Thr Ile Ser 255 1469 gaa tcc agt att agt gac cgg ctt gtc aca ttg gag tcc tgg gct aat Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu Glu Ser Trp Ala Asn 270 1517 gat cct gat tat ctg aaa cgt caa gtt ggt ttc tgt gcc cag tgg agc Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe Cys Ala Gln Trp Ser 290 285 tta gac aat ctc ttt tta aaa gaa ggt aga cag ctg acc tat gag aaa 1565 Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln Leu Thr Tyr Glu Lys 300 305 gtg aac ttg agt agc att agg gcc atg ctg aat agc aat gat gtc agc 1613 Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn Ser Asn Asp Val Ser 315 gag tac ctg aag atc tca cct cat ggc tta gag gct cgc tgt gat gcc 1661 Glu Tyr Leu Lys Ile Ser Pro His Gly Leu Glu Ala Arg Cys Asp Ala 330 335 tcc tct ttt gaa agt gtg cgt tgc acc ttt tgt gtg gat gcc ggg gta 1709 Ser Ser Phe Glu Ser Val Arg Cys Thr Phe Cys Val Asp Ala Gly Val 345 350 355 tgg tac tat gaa gta aca gtg gtc act tct ggc gtc atg cag att ggc 1757 Trp Tyr Tyr Glu Val Thr Val Val Thr Ser Gly Val Met Gln Ile Gly

370

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	tgg Trp															193
	ctc Leu															241
	gtg Val															289
	tgc Cys															337
	aca Thr 110															385
-	act Thr					_	_	-	-	_	_		_	_	-	433
	cac His												tga *	ggag	ggtt	482
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				agg Arg												242
				cag Gln 80												290
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				cct Pro												434
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484

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cat gcg cgc ctg agg gcc ctg aac ggc ctc ctc tat aag gca ctg aca His Ala Arg Leu Arg Ala Leu Asn Gly Leu Leu Tyr Lys Ala Leu Thr 90 95 100 105	340
gac ctg ctg tgt acc cct gaa gtg agt cag gag ctg tat gac ctt aac Asp Leu Leu Cys Thr Pro Glu Val Ser Gln Glu Leu Tyr Asp Leu Asn 110 115 120	388

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Val Glu Leu Ser Lys Val Ser Leu Thr Pro Asp Phe Ser Ala Cys Arg

gcg tac tgg aag aca acg ctc tct gct gag cag aac gca cac atg gag

130

Ala T	Гуr	Trp 140	Lys	Thr	Thr	Leu	Ser 145	Ala	Glu	Gln	Asn	Ala 150	His	Met	Glu	
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gag t Glu T 250						-						_			-	820
ggg c	_		-		_		_	_	_		_					868
gcc a Ala L	_		-	_		_	-	_			_	_		_		916
ggc g Gly G	lu															964
gaa t Glu C 3	_		_	_	-				_		_		_			1012
ggc a Gly A 330														tag *	atg	1060
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gtc aac ctc att gcc tgc ctg gcc tgg tgg atc ggc gga ggc tcg ggg Val Asn Leu Ile Ala Cys Leu Ala Trp Trp Ile Gly Gly Gly Ser Gly 55 60 65	306
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acc ccc cgc gac ggg ggc ccc gtc aac atc ttt cgg cga agc ttg ccc Thr Pro Arg Asp Gly Gly Pro Val Asn Ile Phe Arg Arg Ser Leu Pro 200 205 210	738
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				gga Gly						603
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				tct Ser						699
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				aag Lys						843
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		_	_	gac Asp						939
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	 _			gag Glu 290	_	_	_			1035

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						cca Pro										1851
_		_				cag Gln		~ ~		_	_		_		_	1899
-	_					ccc Pro		_		_						1947
		_	_	_		gat Asp 610										1995
						aga Arg										2043
						cag Gln										2091
						tat Tyr										2139
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						aac Asn										2283
					-	cct Pro										2331
						cag Gln										2379
						aag Lys										2427

755 760 750 aaa aaa cta gcc aag aat ctc ctt aag gag cca gaa aac tgc aac aac 2475 Lys Lys Leu Ala Lys Asn Leu Leu Lys Glu Pro Glu Asn Cys Asn Asn 770 ttt tgc ctg tgg aag cag tat gca cat ctg gag tgg ttg ctt ggc aac 2523 Phe Cys Leu Trp Lys Gln Tyr Ala His Leu Glu Trp Leu Leu Gly Asn 790 785 2571 acg gag gat gcc aga aaa gtt ttt gac aca gca ctt ggc atg gca gga Thr Glu Asp Ala Arg Lys Val Phe Asp Thr Ala Leu Gly Met Ala Gly 800 805 agc aga gaa ctg aaa gac tct gac ctc tgt gag ctc agt ctg ctc tat 2619 Ser Arg Glu Leu Lys Asp Ser Asp Leu Cys Glu Leu Ser Leu Leu Tyr 820 gct gag ctg gag gtg gag ctg tcg cca gaa gtg aga agg gct gcc aca 2667 Ala Glu Leu Glu Val Glu Leu Ser Pro Glu Val Arg Arg Ala Ala Thr 830 835 840 gct cga gct gtt cac ata tta acc aag ctg act gag agc agc ccc tat 2715 Ala Arg Ala Val His Ile Leu Thr Lys Leu Thr Glu Ser Ser Pro Tyr 850 ggg ccc tac act gga cag gtg ttg gct gtt cac att ttg aaa gcg cga 2763 Gly Pro Tyr Thr Gly Gln Val Leu Ala Val His Ile Leu Lys Ala Arg 865 aag get tat gag cac gea etg cag gac tgt ttg ggt gac age tgt gte 2811 Lys Ala Tyr Glu His Ala Leu Gln Asp Cys Leu Gly Asp Ser Cys Val 880 885 tcc aat cca gct ccc acc gat tcc tgt agc cgc cta att agc ctg gct 2859 Ser Asn Pro Ala Pro Thr Asp Ser Cys Ser Arg Leu Ile Ser Leu Ala 895 900 aaa tgc ttc atg ctc ttc cag tat ttg acc ata ggg att gat gct gct 2907 Lys Cys Phe Met Leu Phe Gln Tyr Leu Thr Ile Gly Ile Asp Ala Ala 910 915 gtg cag ata tac gaa cag gtg ttt gca aaa ctg aac agt tct gtt ttc 2955 Val Gln Ile Tyr Glu Gln Val Phe Ala Lys Leu Asn Ser Ser Val Phe 925 930 cca gaa ggc tct ggc gag ggg gac agt gcc agc tcc cag agt tgg acc 3003 Pro Glu Gly Ser Gly Glu Gly Asp Ser Ala Ser Ser Gln Ser Trp Thr 940 945 955 agt gtt ctc gaa gcc atc aca ctg atg cac acg agc ctg ctg aga ttc 3051 Ser Val Leu Glu Ala Ile Thr Leu Met His Thr Ser Leu Leu Arg Phe 970 960 3099 cac atg aaa gtg agt gtt tac ccg ctg gcc cct ctg cga gag gca ctc

His Met Lys Val Ser Val Tyr Pro Leu Ala Pro Leu Arg Glu Ala Leu

980

975

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ttt ttt gac aca atc acc agg tct gcc aaa ccc ttg gag cct tgg ttg Phe Phe Asp Thr Ile Thr Arg Ser Ala Lys Pro Leu Glu Pro Trp Leu 1020 1025 1030 1035	3243
ttt gca att gaa gct gag aaa ctg agg aag aga ctg gtg gaa act gtc Phe Ala Ile Glu Ala Glu Lys Leu Arg Lys Arg Leu Val Glu Thr Val 1040 1045 1050	3291
cag agg tta gac ggt aga gag atc cac gcc aca att cct gag acc ggc Gln Arg Leu Asp Gly Arg Glu Ile His Ala Thr Ile Pro Glu Thr Gly 1055 1060 1065	3339
tta atg cat cgg atc caa gcc ctg ttt gaa aat gcc atg cgc agc gac Leu Met His Arg Ile Gln Ala Leu Phe Glu Asn Ala Met Arg Ser Asp 1070 1075 1080	3387
agt ggc agc cag tgc ccc ttg ctg tgg agg atg tat ttg aac ttt ctg Ser Gly Ser Gln Cys Pro Leu Leu Trp Arg Met Tyr Leu Asn Phe Leu 1085 1090 1095	3435
gtt tcc tta gga aat aaa gaa aga agc aaa ggt gta ttc tac aaa gca Val Ser Leu Gly Asn Lys Glu Arg Ser Lys Gly Val Phe Tyr Lys Ala 1100 1105 1110 1115	3483
ctt cag aat tgc cct tgg gca aag gtg ttg tac ctg gac gcc gtg gag Leu Gln Asn Cys Pro Trp Ala Lys Val Leu Tyr Leu Asp Ala Val Glu 1120 1125 1130	3531
tat ttc ccc gat gag atg cag gag atc ctg gac ctg atg act gag aag Tyr Phe Pro Asp Glu Met Gln Glu Ile Leu Asp Leu Met Thr Glu Lys 1135 1140 1145	3579
gag ctc cgg gtg cgc ctg ccg ctg gag gag ctg gag ctg ctg ctg gag Glu Leu Arg Val Arg Leu Pro Leu Glu Glu Leu Glu Leu Leu Glu 1150 1155 1160	3627
gat tag agagcagtgg gaaaacgggc tgtgcctgcg aggccaagtt gcccaccctg Asp * 1165	3683
cggagctagg aggcgcgagc agagaacgtg tgtgttagga gaactcggct tttgaaatgt	3743
tetttetega tagtaataat gtgggetgee ageeteteae atettgeaea etttttgggt	3803
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ctt gag att tca aga att ttg aat act ggc tta gat atg gaa act ctg Leu Glu Ile Ser Arg Ile Leu Asn Thr Gly Leu Asp Met Glu Thr Leu 30 35 40	145
tct att tgt gta cgg ctt tgt gaa caa gga att aac cca gaa gct tta Ser Ile Cys Val Arg Leu Cys Glu Gln Gly Ile Asn Pro Glu Ala Leu 45 50 55 60	193
tca tcg gtt att aag gag ctt cgc aag gct act gaa gca ctg aag gct Ser Ser Val Ile Lys Glu Leu Arg Lys Ala Thr Glu Ala Leu Lys Ala 65 70 75	241
gct gaa aat atg aca agc tga ct ttctggagaa attctgatga gatatgtcaa Ala Glu Asn Met Thr Ser * 80	294
gctctgcaag agggttagaa gattgcattg tagttgagaa tgtacaatga aattactgca	354
tgcagcagtg tagaaaaatt ttacttttta aaagaattat aaaaccatag ctttataaat	414
cagtggaaag tggcttacag agagaactat cagatgtgtt tacatcacat cttattcact	474
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tagctctgat agctttaatt ttctaagcag tctgtctatc agatgtgcac atctgctgtg	594
ccaggttgaa gtatagtgga acccatcagt agtaatgtgt agtagttatg acttgttgac	654
atttccatta taaactttaa ttttgaattg tttatgcatt ataactgtgg atttatattg	714
tattgggctg aaagttgaca ggatttcagc caccacttgt gaatttttat ttagattcat	774
tatgtatatc agaatcttgt tttttgaaat aagagcatgg aaaacatttc ttgtaatcta	834
ctcttgaaca aagaatattt agtttttcaa acagtttgtt gggcagctaa tagtgtgaac	894

caggtcattt ttgtattgag taaaaaaatc aaactttgag aaacttggat tttaaaagta 954
atgacaatgc ttaggttagt attatttgta atttgaatca tttacatcta atgagaatgt 1014
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																cag Gln	625
_		•			_	gag Glu		_							_	gga Gly	673
	_					acc Thr			-		_	_	_				721
_	-			_		cta Leu			_				-	_		_	769
$\mathbf{T}$					_	cca Pro 180					_	_		-		-	817
		_	_			agg Arg		_	_	_	-	_	_		_		865
			-			cct Pro	_	_	_				_				913
			-			gtc Val	-	-		_			_		_	_	961
_		_		_	_	acc Thr		_	-		_	~			_	•	1009
V						aat Asn 260											1057
						gca Ala											1105
						gag Glu											1153
		Leu				gtc Val											1201
	lu					tgc Cys											1249
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					cac His											1345
ctg Leu	aaa Lys	Gly	ctg Leu 370	tac Tyr	ggt Gly	aac Asn	cgg Arg	gac Asp 375	ctg Leu	acc Thr	gca Ala	cgc Arg	ctg Leu 380	gag Glu	ctc Leu	1393
					aag Lys											1441
gag Glu	tac Tyr 400	agt Ser	gtg Val	gca Ala	gtg Val	gag Glu 405	gcc Ala	gtc Val	aga Arg	tta Leu	ctg Leu 410	ata Ile	ctt Leu	ata Ile	ctt Leu	1489
					ttg Leu 420											1537
					tct Ser											1585
ttt Phe	ctg Leu	tac Tyr	tgg Trp 450	aaa Lys	ctt Leu	ttc Phe	tac Tyr	cct Pro 455	gag Glu	tgc Cys	gag Glu	ata Ile	aga Arg 460	acg Thr	atg Met	1633
					cgc Arg											1681
					ttc Phe											1729
					agt Ser 500											1777
					aca Thr											1825
					agc Ser											1873
					Gly ggg											1921
aag Lys	ggc Gly	tta Leu	acc Thr	tct Ser	aag Lys	gag Glu	cgc Arg	aag Lys	acc Thr	caa Gln	gcc Ala	gat Asp	gac Asp	agg Arg	gtg Val	1969

560 565 570

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					gag Glu											2065
					atc Ile											2113
					caa Gln											2161
cca Pro	gcg Ala 640	gtg Val	ctt Leu	gag Glu	gct Ala	ggg Gly 645	gcg Ala	cat His	gcc Ala	ctc Leu	tac Tyr 650	ctg Leu	ctc Leu	tgt Cys	aat Asn	2209
					ttc Phe 660											2257
gta Val	gat Asp	ttg Leu	ctg Leu	act Thr 675	gac Asp	cgc Arg	ttc Phe	cag Gln	cag Gln 680	gag Glu	ctt Leu	gaa Glu	gag Glu	ctg Leu 685	tta Leu	2305
					gat Asp											2353
					gcc Ala											2401
					tgt Cys											2449
gga Gly 735	gag Glu	gtt Val	cct Pro	cac His	cag Gln 740	gtt Val	atc Ile	ctg Leu	cca Pro	gcc Ala 745	ttg Leu	act Thr	ctt Leu	gtc Val	tat Tyr 750	2497
					aca Thr											2545
cag Gln	aag Lys	cag Gln	ctg Leu 770	tcg Ser	agt Ser	ttg Leu	agg Arg	gac Asp 775	aga Arg	atg Met	gtg Val	gcc Ala	ttc Phe 780	tgt Cys	gaa Glu	2593
					ctc Leu											2641

_		_			-	_						agc Ser				2689
												ttt Phe				2737
												gac Asp				2785
	_	_		_	_		_		_		-	gag Glu	-			2833
												gcc Ala 875				2881
-	_	-					_		_	-		gcc Ala		_	-	2929
					_				-			gac Asp			_	2977
_				_	_		_		_	-	-	cat His	-		_	3025
												ctg Leu				3073
			_		_					_		atc Ile 955		_		3121
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_						-		Ser			_	cct Pro	Pro		_	3265
-		Leu					Glu				-	ctc Leu 1			_	3313

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tec cag gea cet gge cat eec tgg gge eea gte ace ace tae tge cae Ser Gln Ala Pro Gly His Pro Trp Gly Pro Val Thr Thr Tyr Cys His 1040 1045 1050	3409
tcc ctc agc cct gtg gag aac aca gca gag acc agc cct cag gtc ctc Ser Leu Ser Pro Val Glu Asn Thr Ala Glu Thr Ser Pro Gln Val Leu 1055 1060 1065 1070	3457
ccc agc tcc aag agg agg cgc gtt gaa ggg cct gcc aag cct aac aga Pro Ser Ser Lys Arg Arg Arg Val Glu Gly Pro Ala Lys Pro Asn Arg 1075 1080 1085	3505
gag gac gtc tcc tcg tcc cag gaa gaa agt ctg cag ctg aac agc atc Glu Asp Val Ser Ser Ser Gln Glu Glu Ser Leu Gln Leu Asn Ser Ile 1090 1095 1100	3553
ccg ccc acg ccc acc ctc acc tcc aca gct gtg aag agc agg cag ccc Pro Pro Thr Pro Thr Leu Thr Ser Thr Ala Val Lys Ser Arg Gln Pro 1105 1110 1115	3601
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ttt gcc cag ggc agt cag ccc gtc gca ggc acc gag agg tca agg ttc Phe Ala Gln Gly Ser Gln Pro Val Ala Gly Thr Glu Arg Ser Arg Phe 1135 1140 1145 1150	3697
ttg ggt cca caa tat ttc cag act cca cac aac cct tca ggt cct ggc Leu Gly Pro Gln Tyr Phe Gln Thr Pro His Asn Pro Ser Gly Pro Gly 1155 1160 1165	3745
ctg ggc aac cag ctg atg cga ctc agc ctt atg gaa gag gac gag gaa Leu Gly Asn Gln Leu Met Arg Leu Ser Leu Met Glu Glu Asp Glu Glu 1170 1175 1180	3793
gaa gag tta gaa atc cag gat gag tca aat gaa gaa cgg cag gat aca Glu Glu Leu Glu Ile Gln Asp Glu Ser Asn Glu Glu Arg Gln Asp Thr 1185 1190 1195	3841
gac atg caa gca agt agc tac tct tcc acc agt gag cgc ggg ctg gac Asp Met Gln Ala Ser Ser Tyr Ser Ser Thr Ser Glu Arg Gly Leu Asp 1200 1205 1210	3889
ctc tta gat tct aca gag ctg gat att gag gat ttc tga caggactctg Leu Leu Asp Ser Thr Glu Leu Asp Ile Glu Asp Phe * 1215 1220 1225	3938
ggcccctccc cagctccact ccctacctca agaatgtgac catttggaaa aggcaaagag	3998
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tgggcattgt ttttctaacc taacctttcc ctctggggta gagaagccga gagaccctgt	4118

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aagggcagca	cctctgtgtt	taatggaaat	agcccatagt	ctcctggatt	tttggaacat	4238
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tcc Ser	ttg Leu	cag Gln	caa Gln 140	cgg Arg	ctc Leu	cag Gln	tgc Cys	atg Met 145	atg Met	agg Arg	gct Ala	ggc Gly	acc Thr 150	acg Thr	ctg Leu	484
gtg Val	gag Glu	tgc Cys 155	aag Lys	agt Ser	gga Gly	tat Tyr	ggc Gly 160	ctc Leu	gac Asp	ctg Leu	gag Glu	acc Thr 165	gag Glu	ctc Leu	aag Lys	532
atg Met	ctg Leu 170	cgc Arg	gtg Val	att Ile	gag Glu	cgc Arg 175	gcc Ala	cgg Arg	cgg Arg	gag Glu	ctg Leu 180	gac Asp	atc Ile	ggc Gly	atc Ile	580
tcg Ser 185	gct Ala	acc Thr	tac Tyr	tgc Cys	ggg Gly 190	gct Ala	cat His	tca Ser	gtg Val	cct Pro 195	aaa Lys	gga Gly	aaa Lys	act Thr	gct Ala 200	628
act Thr	gaa Glu	gct Ala	gct Ala	gat Asp 205	gac Asp	atc Ile	atc Ile	aat Asn	aac Asn 210	cac His	ctc Leu	cca Pro	aag Lys	ctg Leu 215	aag Lys	676
gaa Glu	ctt Leu	ggc Gly	aga Arg 220	aat Asn	gly ggg	gaa Glu	ata Ile	cac His 225	gtg Val	gac Asp	aat Asn	ata Ile	gac Asp 230	gta Val	ttt Phe	724
tgt Cys	gag Glu	aaa Lys 235	ggt Gly	gtc Val	ttt Phe	gat Asp	ctc Leu 240	gat Asp	tcc Ser	acc Thr	aga Arg	agg Arg 245	att Ile	ctt Leu	caa Gln	772
cgt Arg	gga Gly 250	aaa Lys	gat Asp	ata Ile	Gly	tta Leu 255	cag Gln	att Ile	aac Asn	ttc Phe	cat His 260	ggg Gly	gat Asp	gaa Glu	ctc Leu	820
cac His 265	ccg Pro	atg Met	aag Lys	gct Ala	gct Ala 270	gag Glu	ctt Leu	ggg Gly	gct Ala	gaa Glu 275	ctg Leu	gga Gly	gcg Ala	cag Gln	gca Ala 280	868
atc Ile	agc Ser	cac His	ctg Leu	gaa Glu 285	gaa Glu	gtg Val	agt Ser	gat Asp	gaa Glu 290	ggc Gly	atc Ile	gtt Val	gcc Ala	atg Met 295	gca Ala	916
acg Thr	gcc Ala	agg Arg	tgc Cys 300	tct Ser	gcc Ala	atc Ile	ctt Leu	ctg Leu 305	ccc Pro	acc Thr	aca Thr	gcc Ala	tac Tyr 310	atg Met	ctg Leu	964
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gtt Val	gct Ala 330	ctg Leu	gga Gly	agt Ser	gat Asp	ttc Phe 335	aac Asn	ccc Pro	aat Asn	gca Ala	tat Tyr 340	tgc Cys	ttt Phe	tca Ser	atg Met	1060
cca Pro 345	atg Met	gtc Val	atg Met	cat His	ctg Leu 350	gcc Ala	tgt Cys	gta Val	aac Asn	atg Met 355	aga Arg	atg Met	tcc Ser	atg Met	cct Pro 360	1108

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cat cat gaa tta att gaa tat gtt ata gct aaa gga aaa ctc atc tat His His Glu Leu Ile Glu Tyr Val Ile Ala Lys Gly Lys Leu Ile Tyr 410 415 420	1300
aaa aca tga tagattt gaaaagagaa gactttttga ctatatgaaa taagtcaata Lys Thr * 425	1356
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aaa gaa aaa cag ctc gag acc tca tgc aaa gag aaa act gag tat cta Lys Glu Lys Gln Leu Glu Thr Ser Cys Lys Glu Lys Thr Glu Tyr Leu 15 20 25	336

						aat Asn					Gln					384
		_		-	-	cat His		-				_		~	•	432
					-	tat Tyr	_		_	_	_	_		_	-	480
			-	_	_	cga Arg		_	-		-	_				528
						aca Thr 100										576
			_		_	cga Arg			-	_	_		_		_	624
						aaa Lys										672
						ctt Leu										720
			_	-	_	agg Arg	_					-		_		768
						cta Leu 180										816
						att Ile										864
						ggc Gly	_			-	_	_	-			912
						aaa Lys										960
	Asp					cag Gln					Leu					1008
cgt	gac	acg	tat	gat	gct	gtt	tta	tgg	cta	aga	aat	aac	aga	gac	aaa	1056

Arg	Asp 255	Thr	Tyr	Asp	Ala	Val 260	Leu	Trp	Leu	Arg	Asn 265	Asn	Arg	Asp	Lys		
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														ttc Phe		120	0
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														aat Asn		129	6
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gtt Val	cct Pro	gta Val	gga Gly 385	act Thr	gaa Glu	aag Lys	acc Thr	aga Arg 390	gaa Glu	aga Arg	att Ile	gaa Glu	cgg Arg 395	gta Val	ata Ile	144	0
														tat Tyr		148	8
gtg Val	aaa Lys 415	act Thr	tct Ser	ttt Phe	tat Tyr	tca Ser 420	aac Asn	aaa Lys	gtt Val	att Ile	tct Ser 425	agt Ser	aac Asn	aca Thr	tct Ser	153	6
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aga Arg	cac His	tta Leu	gaa Glu	gaa Glu 450	cag Gln	cta Leu	aag Lys	gaa Glu	att Ile 455	cat His	aga Arg	aaa Lys	ttg Leu	caa Gln 460	gca Ala	163	2
gtg Val	gat Asp	tca Ser	ggg Gly 465	ttg Leu	att Ile	gcc Ala	tta Leu	cgt Arg 470	gaa Glu	aca Thr	agc Ser	aaa Lys	cat His 475	ctg Leu	gag Glu	168	0
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485 490 480 1776 aaa acc aag aaa aga caa ctg gaa caa aaa atc agt tcc aaa cta gga Lys Thr Lys Lys Arg Gln Leu Glu Gln Lys Ile Ser Ser Lys Leu Gly 500 1824 agt tta aag ctg atg gaa cag gat act tgc aat ctt gaa gag gaa gag Ser Leu Lys Leu Met Glu Gln Asp Thr Cys Asn Leu Glu Glu Glu Glu 515 1872 cqa aaa qca aqt acc aaa atc aaa gaa ata aat gtt caa aaa gcg aaa Arg Lys Ala Ser Thr Lys Ile Lys Glu Ile Asn Val Gln Lys Ala Lys 535 530 1920 ctt qtt acc qaa tta aca aac cta ata aag att tgt act tct ttg cat Leu Val Thr Glu Leu Thr Asn Leu Ile Lys Ile Cys Thr Ser Leu His 545 550 1968 ata caa aaa gta gat tta att ctc caa aat act aca gtg atc tct gag Ile Gln Lys Val Asp Leu Ile Leu Gln Asn Thr Thr Val Ile Ser Glu 560 565 2016 aag aac aaa tta gaa tca gat tat atg gcc gca tct tca caa ctc cgt Lys Asn Lys Leu Glu Ser Asp Tyr Met Ala Ala Ser Ser Gln Leu Arg 580 2064 ctt aca gag caa cat ttc att gaa ttg gat gaa aat aga cag aga tta Leu Thr Glu Gln His Phe Ile Glu Leu Asp Glu Asn Arg Gln Arg Leu 595 2112 ttg cag aaa tgc aag gaa ctt atg aaa aga gct agg caa gta tgt aac Leu Gln Lys Cys Lys Glu Leu Met Lys Arg Ala Arg Gln Val Cys Asn 610 ctg ggt gca gag cag act ctt cct caa gaa tac cag aca caa gta ccc 2160 Leu Gly Ala Glu Gln Thr Leu Pro Gln Glu Tyr Gln Thr Gln Val Pro 625 630 2208 acc att cca aat gga cac aac tcc tca ctc ccc atg gtt ttc caa gac Thr Ile Pro Asn Gly His Asn Ser Ser Leu Pro Met Val Phe Gln Asp 640 645 2256 ctt cca aac aca ttg gat gaa att gat gct tta tta act gaa gaa aga Leu Pro Asn Thr Leu Asp Glu Ile Asp Ala Leu Leu Thr Glu Glu Arg 655 660 2304 tca aga gct tcc tgc ttc acg gga ctg aat cct aca att gtt cag gaa Ser Arg Ala Ser Cys Phe Thr Gly Leu Asn Pro Thr Ile Val Gln Glu 685 670 675 2358 tat aca aaa aaa aaa aaa tag aacagttaac tgaggaacta aagggaaaga Tyr Thr Lys Lys Lys Lys 690

2418

2478

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<sup>&</sup>lt;210> 35

<sup>&</sup>lt;211> 3596

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (103)..(3084)

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ggc ctc ccc agg ttt cac tcc gtt tct aca cag tcg gag ccc cat gga Gly Leu Pro Arg Phe His Ser Val Ser Thr Gln Ser Glu Pro His Gly 25 30 35	210
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gag aag cag gct act ctg gag gct gag ata gca ggg gag agc aag tca Glu Lys Gln Ala Thr Leu Glu Ala Glu Ile Ala Gly Glu Ser Lys Ser 55 60 65	306
cct gca gaa tcc att aag gcc tgg agg cct aag gag tta gta ttg tat Pro Ala Glu Ser Ile Lys Ala Trp Arg Pro Lys Glu Leu Val Leu Tyr 70 75 80	354
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cct cct gca tac agc ccc cga tat gtt gag gct gcc tgg tac ccg tgg Pro Pro Ala Tyr Ser Pro Arg Tyr Val Glu Ala Ala Trp Tyr Pro Trp 105 110 115	450
tgg gta cga gag ggc ttc ttc aaa cca gaa tat cag gcc cgg ctg ccc Trp Val Arg Glu Gly Phe Phe Lys Pro Glu Tyr Gln Ala Arg Leu Pro 120 125 130	498
caa gct aca ggg gag acc ttt tcc atg tgt atc cca cct ccc aat gtc Gln Ala Thr Gly Glu Thr Phe Ser Met Cys Ile Pro Pro Pro Asn Val 135 140 145	546
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cct ggt tca gat cat gca gga att gct aca caa gct gtg gtg gag aaa Pro Gly Ser Asp His Ala Gly Ile Ala Thr Gln Ala Val Val Glu Lys 185 190 195	690
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1074	act Thr	gtg Val	aag Lys	gtg Val	gca Ala 320	ggg Gly	acg Thr	ggc Gly	gtg Val	cat His 315	cca Pro	cag Gln	gtt Val	gct Ala	tat Tyr 310	gac Asp
1122	ttg Leu 340	ggc Gly	cat His	cga Arg	gcc Ala	ggg Gly 335	atg Met	gag Glu	gct Ala	gat Asp	gcc Ala 330	cct Pro	agt Ser	cac His	gct Ala	cca Pro 325
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1266	cac His	aac Asn	cag Gln	ctc Leu 385	ggc Gly	cgg Arg	ttc Phe	ctg Leu	ggc Gly 380	cgg Arg	gaa Glu	agt Ser	ctg Leu	gtg Val 375	tct Ser	atg Met
1314	tac Tyr	gaa Glu	ata Ile	gtg Val	gat Asp 400	ggg	tct Ser	cgt Arg	agc Ser	tgc Cys 395	atc Ile	ccc Pro	ctg Leu	Val	atg Met 390	ccc Pro
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1410	ttc Phe	tcc Ser	ccc Pro	agt Ser	ctc Leu	gag Glu	ctg Leu	gcc Ala	ggg Gly	tcg Ser	gag Glu	gtg Val	gct Ala	aag Lys	gcc Ala	gct Ala

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	aag Lys															217
	ttt Phe			_		_	-		~					-	-	222
-	gcc Ala 710			-	-	-		_	_	-						227
	ggc Gly															232
	ttc Phe						_	-	-		_		_		_	237
	gtg Val															241
	tcc Ser	_	_	-				-		_	-		_	_		246
	ctg Leu 790	-	-				_		_						_	251
	cct Pro	-		_		_	_	_				_	-	_	_	256
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	gag Glu															265
	aaa Lys	~			_		_	_	_	_					-	270
	ggc Gly 870															275

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<210> 36
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<sup>&</sup>lt;211> 1406

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (555)..(1406)

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105

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						ctt Leu 40										201
	_					ttt Phe				-				_	_	249
						aac Asn										297
		_		_	_	ttt Phe		_	_	_				_		345
	_	-	_	-		gtc Val			_	_		_			-	393
						ctg Leu 120										441
						ctg Leu										489
-	_					ctg Leu	-			-		_	-	_		537
				-		ctg Leu			_	_				_	_	585
_			_	_	_	ctc Leu	_		-	-						633
						ctg Leu 200										681
						ctg Leu										729
						ctg Leu										777
tgc	cta	gag	agg	ctg	tgg	ctg	caa	cgc	aac	gcc	atc	acg	cac	ctg	ccg	825

Cys	Leu	Glu	Arg 245	Leu	Trp	Leu	Gln	Arg 250	Asn	Ala	Ile	Thr	His 255	Leu	Pro	
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														acc Thr		921
														gtc Val		969
														ctc Leu 320		1017
														ctg Leu		1065
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														ctc Leu		1161
														aac Asn		1209
														gac Asp 400		1257
cac His	ctg Leu	gcc Ala	tac Tyr 405	ctc Leu	ttc Phe	aac Asn	tgg Trp	ctg Leu 410	cag Gln	cag Gln	tac Tyr	acc Thr	gat Asp 415	cgg Arg	ctc Leu	1305
														ggc Gly		1353
														acc Thr		1401
														gca Ala		1449
ggc Gly	agc Ser	tgg Trp	gat Asp	ctg Leu	gct Ala	gtg Val	cag Gln	gaa Glu	agg Arg	gca Ala	gcc Ala	cgg Arg	agc Ser	cag Gln	tgc Cys	1497

480 470 475 1545 acc tac agc aac ccc gag ggc acc gtg gtg ctc gcc tgt gac cag gcc Thr Tyr Ser Asn Pro Glu Gly Thr Val Val Leu Ala Cys Asp Gln Ala 490 485 1593 cag tgt cgc tgg ctg aac gtc cag ctc tct cct cgg cag ggc tcc ctg Gln Cys Arg Trp Leu Asn Val Gln Leu Ser Pro Arg Gln Gly Ser Leu 500 505 1641 gga ctg cag tac aat gct agt cag gag tgg gac ctg agg tcg agc tgc Gly Leu Gln Tyr Asn Ala Ser Gln Glu Trp Asp Leu Arg Ser Ser Cys 520 515 1689 ggt tet etg egg etc ace gtg tet ate gag get egg gea gea ggg ece Gly Ser Leu Arg Leu Thr Val Ser Ile Glu Ala Arg Ala Ala Gly Pro 540 530 535 1746 tag tagc agcgcataca ggagctgggg aagggggcct ctggggcctg accaggcgac aggtaggggc ggaggggagc tgagtctccg aagccttggc ttttcacatg caagggacag 1806 1866 ggttacatcc ccaaggtgag ggggtggagt ctggtctgct ccactaacca gggtctcctc 1926 ctcctcttcc ttcatcgctt ctcctggagt gtgcggccta acaaggccat ccttatgctt tgcaaagcac cctcaaaagc tgcaccacag cctggagaat aaaatatcct cagccctgat 1986 2046 gcctccccat tatgtaacac ccaaccgctc tcacctacac cctgaggtct attcactgca tcccagtgat acaaagtgga ggccactgcc ttctgacatc tggctcaaaa gcccagtgtc 2106 2166 tgtttccatt tatttccctg gaatttcatt taaaattggt atagagaaaa aaaggatgtg acagaagcag agatgaccag aaagcacagg ggcagggttc tgactggcgt gtgggagacc 2226 ctgtggccgg cacccacctc cacacgagga ctaagctctg attttttat cttgcccaaa 2286 ttcctaccta aggggtctag ggagtcgcgc cttacaaatc ataaattctc atcagatggg 2346 2406 ttttatttga ccctgtatat catgacttat ttttaatctg actatggcat aacattacaa gacgaggcaa aaatatttaa cccccaaata tatttctttg ccctaccttg aacttgccct 2466 gcagagtctc ttgtgaggag aatccacatc ctataaagaa gcccctttcc cctttgtttt 2526 ccttcctttc tttccagtcc aggagatcat caactaagag ccaggcaccc cttttaagtc 2586 gataagaaac agtttacaac ctgctctctc tctctctgaa gtctgctgag agcttcccct 2646 gcacaataaa acttggcctc cacgatcctt tatcttaacc tgaacattcc tttccattga 2706 2766 tcccaggtct tcagctaagc tcaaccaatt gtcaaccaga aaatgtttaa atttacctac agcctggaag cacccaccc cgctgcttcg agttgtcctg cctttctgaa ctcaaccaat 2826 gtatttetta aatgtatttg attgatgeet catteeteec taaaatgtat aaaaccaage 2886
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1 5 10

cag cct ccc aac tac gag atg ctc aag gag gag cag gaa gtg gct atg

Gln Pro Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met

15 20 25 30

ctg ggg gtg ccc cac aac cct gct ccc ccg atg tcc acc gtg atc cac

Leu Gly Val Pro His Asn Pro Ala Pro Pro Met Ser Thr Val Ile His

atc cgc agc gag acc tcc gtg cct gac cat gtg gtc tgg tcc ctg ttc

253

Ile Arg Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe

50

55

60

aac acc ctc ttc atg aac acc tgc tgc ctg ggc ttc ata gca ttc gcg
Asn Thr Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala
65 70 75

tac tcc gtg aag tct agg gac agg aag atg gtt ggc gac gtg acc ggg
Tyr Ser Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly
80 85 90

gcc cag gcc tat gcc tcc acc gcc aag tgc ctg aac atc tgg gcc ctg
Ala Gln Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu
95 100 105 110

att ttg ggc atc ttc atg acc att ctg ctc atc atc cca gtg ttg Ile Leu Gly Ile Phe Met Thr Ile Leu Leu Ile Ile Pro Val Leu 115 120 125

gtc gtc cag gcc cag cga tag at caggaggcat cattgaggcc aggagctctg 498
Val Val Gln Ala Gln Arg \*

130

cccgtgagct gtatccacgt actctatctt ccattcttcg cctgcccca gaggccagag 558
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gctgcctcgg cggcccggcc cggctcgacg cca atg gtg gag gcc ata gtg gag 294

Met Val Glu Ala Ile Val Glu

ttt gac tac cag gcc cag cac gat gat gag ctg acg atc agc gtg ggt

Phe Asp Tyr Gln Ala Gln His Asp Asp Glu Leu Thr Ile Ser Val Gly

10 15 20

gaa atc atc acc aac atc agg aag gag gat gga ggc tgg tgg gag gga 390
Glu Ile Ile Thr Asn Ile Arg Lys Glu Asp Gly Gly Trp Trp Glu Gly
25 30 35

cag atc aac ggc agg aga ggt ttg ttc cct gac aac ttt gta aga gaa 438 Gln Ile Asn Gly Arg Arg Gly Leu Phe Pro Asp Asn Phe Val Arg Glu 40 45 50 55

ata aag aaa gag atg aag aaa gac cct ctc acc aac aaa gct cca gaa 486

Ile Lys Lys Glu Met Lys Lys Asp Pro Leu Thr Asn Lys Ala Pro Glu
60 65 70

aag ccc ctg cac gaa gtg ccc agt gga aac tct ttg ctg tct tct gaa 534
Lys Pro Leu His Glu Val Pro Ser Gly Asn Ser Leu Leu Ser Ser Glu
75 80 85

acg att tta aga acc aat aag aga ggc gag cga cgg agg cgc cgg tgc 582

Thr Ile Leu Arg Thr Asn Lys Arg Gly Glu Arg Arg Arg Arg Cys
90 95 100

cag gtg gca ttc agc tac ctg ccc cag aat gac gat gaa ctt gag ctg 630

Gln	Val 105	Ala	Phe	Ser	Tyr	Leu 110	Pro	Gln	Asn	Asp	Asp 115	Glu	Leu	Glu	Leu	
aaa Lys 120	gtt Val	ggc Gly	gac Asp	atc Ile	ata Ile 125	gag Glu	gtg Val	gta Val	gga Gly	gag Glu 130	gta Val	gag Glu	gaa Glu	gga Gly	tgg Trp 135	678
tgg Trp	gaa Glu	ggt Gly	gtt Val	ctc Leu 140	aac Asn	gly ggg	aag Lys	act Thr	gga Gly 145	atg Met	ttt Phe	cct Pro	tcc Ser	aac Asn 150	ttc Phe	726
atc Ile	aag Lys	gag Glu	ctg Leu 155	tca Ser	Gly	gag Glu	tcg Ser	gat Asp 160	gag Glu	ctt Leu	ggc Gly	att Ile	tcc Ser 165	cag Gln	gat Asp	774
gag Glu	cag Gln	cta Leu 170	tcc Ser	aag Lys	tca Ser	agt Ser	tta Leu 175	agg Arg	gaa Glu	acc Thr	aca Thr	ggc Gly 180	tcc Ser	gag Glu	agt Ser	822
gat Asp	ggg Gly 185	ggt Gly	gac Asp	tca Ser	agc Ser	agc Ser 190	acc Thr	aag Lys	tct Ser	gaa Glu	ggt Gly 195	gcc Ala	aac Asn	ggg Gly	aca Thr	870
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gga Gly	gac Asp	att Ile	ttc Phe	aaa Lys 220	gac Asp	aag Lys	cca Pro	atc Ile	aaa Lys 225	cta Leu	aga Arg	cca Pro	agg Arg	tca Ser 230	att Ile	966
gaa Glu	gta Val	gaa Glu	aat Asn 235	gac Asp	ttt Phe	ctg Leu	ccg Pro	gta Val 240	gaa Glu	aag Lys	act Thr	att Ile	ggg Gly 245	aag Lys	aag Lys	1014
tta Leu	cct Pro	gca Ala 250	act Thr	aca Thr	gca Ala	act Thr	cca Pro 255	gac Asp	tca Ser	tca Ser	aaa Lys	aca Thr 260	gaa Glu	atg Met	gac Asp	1062
agc Ser	agg Arg 265	aca Thr	aag Lys	agc Ser	aag Lys	gat Asp 270	tac Tyr	tgc Cys	aaa Lys	gta Val	ata Ile 275	ttt Phe	cca Pro	tat Tyr	gag Glu	1110
gca Ala 280	cag Gln	aat Asn	gat Asp	gat Asp	gaa Glu 285	ttg Leu	aca Thr	atc Ile	aaa Lys	gaa Glu 290	gga Gly	gat Asp	ata Ile	gtc Val	act Thr 295	1158
ctc Leu	atc Ile	aat Asn	aag Lys	gac Asp 300	tgc Cys	atc Ile	gac Asp	gta Val	ggc Gly 305	tgg Trp	tgg Trp	gaa Glu	gga Gly	gag Glu 310	ctg Leu	1206
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ccg Pro	gac Asp	ttt Phe	gaa Glu	aag Lys	gaa Glu	ggg Gly	aat Asn	aga Arg	ccc Pro	aag Lys	aag Lys	cca Pro	ccg Pro	cct Pro	cca Pro	1302

		330					335					340					
tcc Ser	gct Ala 345	cct Pro	gtc Val	atc Ile	aaa Lys	caa Gln 350	Gly	gca Ala	ggc Gly	acc Thr	act Thr 355	gag Glu	aga Arg	aaa Lys	cat His	135	0
gaa Glu 360	att Ile	aaa Lys	aag Lys	ata Ile	cct Pro 365	cct Pro	gaa Glu	aga Arg	cca Pro	gaa Glu 370	atg Met	ctt Leu	cca Pro	aac Asn	aga Arg 375	139	8
aca Thr	gaa Glu	gaa Glu	aaa Lys	gaa Glu 380	aga Arg	cca Pro	gag Glu	aga Arg	gag Glu 385	cca Pro	aaa Lys	ctg Leu	gat Asp	tta Leu 390	cag Gln	144	6
aag Lys	ccc Pro	tcc Ser	gtt Val 395	cct Pro	gcc Ala	ata Ile	ccg Pro	cca Pro 400	aaa Lys	aag Lys	cct Pro	cgg Arg	cca Pro 405	cct Pro	aag Lys	149	4
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aga Arg	ccg Pro 425	gtg Val	ggt Gly	ccg Pro	ctg Leu	aca Thr 430	cac His	acc Thr	agg Arg	ggt Gly	gac Asp 435	agt Ser	cca Pro	aag Lys	att Ile	159	0
gac Asp 440	ttg Leu	gcc Ala	ggc Gly	agt Ser	tcg Ser 445	cta Leu	tct Ser	ggc Gly	atc Ile	ctg Leu 450	gac Asp	aaa Lys	gat Asp	ctc Leu	tcg Ser 455	163	8
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Gly	agg Arg	cgg Arg 490	cct Pro	ccg Pro	tcc Ser	cag Gln	tcc Ser 495	ctc Leu	aca Thr	tct Ser	tca Ser	tcc Ser 500	ctt Leu	tca Ser	agc Ser	178	2
cct Pro	gat Asp 505	atc Ile	ttc Phe	gac Asp	tcc Ser	cca Pro 510	agt Ser	ccc Pro	gaa Glu	gag Glu	gat Asp 515	aag Lys	gag Glu	gaa Glu	cac His	183	0
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aag Lys	ccg Pro	Gly	acc Thr 555	atg Met	gca Ala	gca Ala	ggt Gly	ggc Gly 560	ggt Gly	ggg	cca Pro	gcc Ala	cct Pro 565	ctg Leu	tcc Ser	197	4

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gga Gly	gac Asp	att Ile	ttc Phe	aaa Lys 220	gac Asp	aag Lys	cca Pro	atc Ile	aaa Lys 225	cta Leu	aga Arg	cca Pro	agg Arg	tca Ser 230	att Ile	966
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gca Ala 280	cag Gln	aat Asn	gat Asp	gat Asp	gaa Glu 285	ttg Leu	aca Thr	atc Ile	aaa Lys	gaa Glu 290	gga Gly	gat Asp	ata Ile	gtc Val	act Thr 295	1158
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					aga Arg											1542
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gag Glu	cta Leu	agg Arg 570	aca Thr	cag Gln	gtc Val	cgc Arg	gag Glu 575	ctg Leu	agg Arg	agc Ser	atc Ile	atc Ile 580	gag Glu	acc Thr	atg Met	2022
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-	t cta caa to a Leu Gln So 620		atacttgatc a	aatgaaatgt (	cacattattc	2172
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aaaggtttgc	ctcaaaatgt	ccctgtttga	aagattagca	caaaagtctt	gatagcacaa	2292
cacaaattcc	atccaagagg	agaatcttcc	ccagggttta	gtcctggggc	tggcactcgt	2352
tgtgacttac	acagagcaaa	attgtgctaa	aggcttttct	actctgagat	ctcaatgcga	2412
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aaaatgtaat	ttcagattat	tcgtttacaa	gctttataat	tttatgattt	tttaatcgtg	2532
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tgcaattgta	ggttcaacct	gtccctttcc	ctgccagcaa	accccaccac	cctaagagaa	2712
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aatgatctgt	gccttctttt	taccaccctc	ttgattggag	cttttgtgat	gcagctacca	2832
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cagagacaca	gcaagatgcc	cagggagtgc	cgcttcctgg	gctagagaca	agcaccagcc	240
tgcagtggag	aacgcaggac	cccgctgccc	agaaggagca	gccacggcct	gcggaggact	300
ggcccagcaa	ggtcccaggt	cttccctctc	ctcagcgcct	aagagagagg	cccagtgcgg	360

415

Met Phe Arg Lys

gtgaggagtc gcgaggaaga ggcggaaggc gccggaaggc acc atg ttc cgc aag

									cag Gln		463
									ggc Gly 35		511
									aag Lys		559
									atg Met		607
	 -							_	tcg Ser	-	655
_		_	_	_	_	_			acc Thr		703
_	 _	_							ggg Gly 115		751
									cag Gln		799
									tgc Cys		847
									cca Pro		895
									tcc Ser		943
									ctg Leu 195		991
									ggc Gly		1039
									gcc Ala		1087

								gcc Ala								1135
								gag Glu								1183
								gct Ala								1231
								agc Ser 285								1279
								agc Ser								1327
ttg Leu	ccc Pro 310	tcg Ser	gac Asp	cag Gln	ccg Pro	gtg Val 315	ggg ggg	acc Thr	ttc Phe	agc Ser	cct Pro 320	ctg Leu	acc Thr	act Thr	tcg Ser	1375
gat Asp 325	acc Thr	agc Ser	agc Ser	ccc Pro	cag Gln 330	aag Lys	tcc Ser	ctc Leu	cgc Arg	aca Thr 335	gcc Ala	ccg Pro	gcc Ala	aca Thr	ggc Gly 340	1423
cag Gln	ctt Leu	cca Pro	ggc Gly	cgg Arg 345	tct Ser	tcc Ser	cca Pro	gcg Ala	gga Gly 350	tcc Ser	ccc Pro	cgc Arg	acc Thr	tgg Trp 355	cac His	1471
								tac Tyr 365								1519
gcc Ala	aag Lys	ggt Gly 375	gcc Ala	ctg Leu	gct Ala	ggt Gly	gag Glu 380	gac Asp	aca Thr	ggt Gly	gtt Val	gtg Val 385	aca Thr	cat His	gag Glu	1567
cag Gln	ttc Phe 390	aag Lys	gct Ala	gcg Ala	ctc Leu	agg Arg 395	atg Met	gtg Val	gtg Val	gac Asp	cag Gln 400	ggt Gly	gac Asp	ccc Pro	cgg Arg	1615
ctg Leu 405	ctg Leu	ctg Leu	gac Asp	agc Ser	tac Tyr 410	gtg Val	aag Lys	att Ile	ggc Gly	gag Glu 415	ggc Gly	tcc Ser	acc Thr	ggc Gly	atc Ile 420	1663
								tcg Ser								1711
atg Met	atg Met	gac Asp	ctc Leu 440	agg Arg	aag Lys	cag Gln	cag Gln	cgc Arg 445	agg Arg	gag Glu	ctg Leu	ctc Leu	ttc Phe 450	aac Asn	gag Glu	1759

gtg Val	gtg Val	atc Ile 455	atg Met	cgg Arg	gac Asp	tac Tyr	cag Gln 460	cac His	ttc Phe	aac Asn	gtg Val	gtg Val 465	gag Glu	atg Met	tac Tyr	1807
aag Lys	agc Ser 470	tac Tyr	ctg Leu	gtg Val	gga Gly	gag Glu 475	gag Glu	ctg Leu	tgg Trp	gtg Val	ctc Leu 480	atg Met	gag Glu	ttc Phe	ctg Leu	1855
cag Gln 485	gga Gly	gga Gly	gcc Ala	ctc Leu	aca Thr 490	gac Asp	atc Ile	gtc Val	tcc Ser	caa Gln 495	gtc Val	agg Arg	ctg Leu	aat Asn	gag Glu 500	1903
gag Glu	cag Gln	att Ile	gcc Ala	act Thr 505	gtg Val	tgt Cys	gag Glu	gct Ala	gtg Val 510	ctg Leu	cag Gln	gcc Ala	ctg Leu	gcc Ala 515	tac Tyr	1951
ctg Leu	cat His	gct Ala	cag Gln 520	ggt Gly	gtc Val	atc Ile	cac His	cgg Arg 525	gac Asp	atc Ile	aag Lys	agt Ser	gac Asp 530	tcc Ser	atc Ile	1999
ctg Leu	ctg Leu	acc Thr 535	ctc Leu	gat Asp	ggc Gly	agg Arg	gtg Val 540	aag Lys	ctc Leu	tcg Ser	gac Asp	ttc Phe 545	gga Gly	ttc Phe	tgt Cys	2047
gct Ala	cag Gln 550	atc Ile	agc Ser	aaa Lys	gac Asp	gtc Val 555	cct Pro	aag Lys	agg Arg	aag Lys	tcc Ser 560	ctg Leu	gtg Val	gga Gly	acc Thr	2095
ccc Pro 565	tac Tyr	tgg Trp	atg Met	gct Ala	cct Pro 570	gaa Glu	gtg Val	atc Ile	tcc Ser	agg Arg 575	tct Ser	ttg Leu	tat Tyr	gcc Ala	act Thr 580	2143
gag Glu	gtg Val	gat Asp	atc Ile	tgg Trp 585	tct Ser	ctg Leu	ggc Gly	atc Ile	atg Met 590	gtg Val	att Ile	gag Glu	atg Met	gta Val 595	gat Asp	2191
Gly	gag Glu	cca Pro	ccg Pro 600	tac Tyr	ttc Phe	agt Ser	gac Asp	tcc Ser 605	cca Pro	gtg Val	caa Gln	gcc Ala	atg Met 610	aag Lys	agg Arg	2239
ctc Leu	cgg Arg	gac Asp 615	agc Ser	ccc Pro	cca Pro	ccc Pro	aag Lys 620	ctg Leu	aaa Lys	aac Asn	tct Ser	cac His 625	aag Lys	gtc Val	tcc Ser	2287
cca Pro	gtg Val 630	ctg Leu	cga Arg	gac Asp	ttc Phe	ctg Leu 635	gag Glu	cgg Arg	atg Met	ctg Leu	gtg Val 640	cgg Arg	gac Asp	ccc Pro	caa Gln	2335
gag Glu 645	aga Arg	gcc Ala	aca Thr	gcc Ala	cag Gln 650	gag Glu	ctc Leu	cta Leu	gac Asp	cac His 655	ccc Pro	ttc Phe	ctg Leu	ctg Leu	cag Gln 660	2383
aca Thr	ggg Gly	cta Leu	cct Pro	gag Glu 665	tgc Cys	ctg Leu	gtg Val	ccc Pro	ctg Leu 670	atc Ile	cag Gln	ctc Leu	tac Tyr	cga Arg 675	aag Lys	2431
cag	acc	tcc	acc	tgc	tga	gcc	cac (	ccca	agta	tg c	ctgc	cacc	t ac	gccc	acag	2485

## Gln Thr Ser Thr Cys \* 680

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tctacaggat	gaccccttga	tatttgcaca	gggatatttc	taagaaacgc	agaggccagc	2725
gttcctggcc	tctgcagcca	acacagtaga	aaaggctgct	gtggttttt	aaaggcagtt	2785
gtccactagt	gtcctaggcc	actgcagagg	gcagactgct	ggtctccaca	gatacctgct	2845
gttctcagct	ccagcttcaa	acctcgagtc	tcgagagggc	cacggggtgg	tttttatgac	2905
cggaatcccg	cttcctccct	cacgtctgat	gtcctgaagg	tgcagtccca	cctgtacagc	2965
ccctccccgc	ccagaactgt	gaatggcctg	ctccaggcca	tggctggggg	cagggagtga	3025
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10 15 20

ttt ctc cgt cag cgg gtg gca ttc ctg gga ctc ttc ttc ata tcc tgt

Phe Leu Arg Gln Arg Val Ala Phe Leu Gly Leu Phe Phe Ile Ser Cys

25 30 35

ctc ctt tta ctt atg tta atc ata gac ttt cga cat tgg agt gct tca 318
Leu Leu Leu Met Leu Ile Ile Asp Phe Arg His Trp Ser Ala Ser
40 45 50 55

tta Leu	cca Pro	cga Arg	gat Asp	agg Arg 60	caa Gln	tac Tyr	gaa Glu	agg Arg	tat Tyr 65	ttg Leu	gct Ala	cga Arg	gta Val	ggg Gly 70	gag Glu	366
ctt Leu	gaa Glu	gct Ala	act Thr 75	gac Asp	act Thr	gaa Glu	gac Asp	cca Pro 80	aat Asn	ctg Leu	aat Asn	tat Tyr	gga Gly 85	ctt Leu	gtt Val	414
gtt Val	gac Asp	tgt Cys 90	ggc Gly	agc Ser	agt Ser	ggt Gly	tcc Ser 95	cgg Arg	att Ile	ttt Phe	gtt Val	tat Tyr 100	ttc Phe	tgg Trp	cca Pro	462
aga Arg	cat His 105	aat Asn	ggg Gly	aac Asn	ccc Pro	cat His 110	gac Asp	ttg Leu	ctg Leu	gac Asp	atc Ile 115	aaa Lys	cag Gln	atg Met	aga Arg	510
gac Asp 120	cgc Arg	aac Asn	agc Ser	caa Gln	cca Pro 125	gtg Val	gtt Val	aaa Lys	aaa Lys	atc Ile 130	aag Lys	cca Pro	gga Gly	atc Ile	tct Ser 135	558
gca Ala	atg Met	gca Ala	gac Asp	act Thr 140	cca Pro	gaa Glu	cat His	gcc Ala	agt Ser 145	gat Asp	tac Tyr	ctt Leu	cgt Arg	cct Pro 150	ctg Leu	606
ctg Leu	agc Ser	ttt Phe	gct Ala 155	gct Ala	gct Ala	cat His	gtg Val	cct Pro 160	gtg Val	aag Lys	aag Lys	cac His	aag Lys 165	gag Glu	acc Thr	654
cct Pro	ctt Leu	tac Tyr 170	atc Ile	ctc Leu	tgc Cys	aca Thr	gca Ala 175	ggc Gly	atg Met	agg Arg	ctt Leu	ctc Leu 180	cct Pro	gag Glu	agg Arg	702
aag Lys	cag Gln 185	ttg Leu	gct Ala	atc Ile	ttg Leu	gct Ala 190	gac Asp	cta Leu	gtg Val	aaa Lys	gat Asp 195	tta Leu	cca Pro	ctg Leu	gag Glu	750
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cag Gln	gaa Glu	ggg ggg	gtt Val	tat Tyr 220	gca Ala	tgg Trp	att Ile	gga Gly	atc Ile 225	aac Asn	ttt Phe	gtt Val	ttg Leu	gga Gly 230	aga Arg	846
ttc Phe	gac Asp	cac His	gag Glu 235	gat Asp	gaa Glu	tca Ser	gat Asp	gct Ala 240	gag Glu	gct Ala	acc Thr	cag Gln	gaa Glu 245	ttg Leu	gca Ala	894
gca Ala	gga Gly	cgg Arg 250	aga Arg	agg Arg	aca Thr	gta Val	ggg Gly 255	ata Ile	ctg Leu	gat Asp	atg Met	gga Gly 260	gga Gly	gcc Ala	tct Ser	942
ctc Leu	caa Gln 265	att Ile	gct Ala	tat Tyr	gaa Glu	gtt Val 270	cct Pro	acc Thr	tca Ser	acc Thr	tct Ser 275	gtc Val	ctt Leu	cct Pro	gca Ala	990

	_	_	_	-	-	-	aag Lys		_	_	_				_		1038
						Thr	gaa Glu										1086
							aac Asn										1134
							aac Asn								_		1182
							cca Pro 350										1230
]							agg Arg										1278
							tgt Cys										1326
							gcc Ala								_		1374
							gag Glu										1422
							cgc Arg 430										1470
Ι							gat Asp										1518
							ggc Gly										1566
							ttt Phe										1614
							ccc Pro										1662
c	ag	ctg	gtg	tat	gac	cga	gag	gtt	cag	tgg	acg	ctg	gga	gcc	att	cta	1710

Gln Leu Val Tyr Asp Arg Glu Val Gln Trp Thr Leu Gly Ala Ile Leu 505 510 515	
tat aaa aca cga ttc tta cca ctc agg gat ctt cgg cag gaa ggt gtc Tyr Lys Thr Arg Phe Leu Pro Leu Arg Asp Leu Arg Gln Glu Gly Val 520 525 530 535	1758
cga caa gcc cat ggt agc tgg ttc cgt ctc tcc ttt gta tac aac cac Arg Gln Ala His Gly Ser Trp Phe Arg Leu Ser Phe Val Tyr Asn His 540 545 550	1806
tat ctc ttc ttt gcc tgt atc ctg gtg gtg cta ctg gcc atc ttc cta Tyr Leu Phe Phe Ala Cys Ile Leu Val Val Leu Leu Ala Ile Phe Leu 555 560 565	1854
tac ctt ctg cgg cta cgc cga att cac cac cga caa aca cga gcc tca Tyr Leu Leu Arg Leu Arg Arg Ile His His Arg Gln Thr Arg Ala Ser 570 575 580	1902
gct cca ttg gac ttg ctg tgg ctt gaa gag gtg gtg ccc atg atg gga Ala Pro Leu Asp Leu Leu Trp Leu Glu Glu Val Val Pro Met Met Gly 585 590 595	1950
gta cag gtg ggg ccg tga Val Gln Val Gly Pro * 600 605	1968
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tttcaattag ttactttttc ttacaaggct gggagaggga gacagaacaa tagaaaaata	180
actggttgat tcatatggag gtcagagtgg aagcaggtgt gagagggtcc cacagaagaa	240
aacatggcag ccaaagtgtt tgagtccacg gtaagtttgg cttggcctta gctgttgcag	300
gagacctgtg aactctgcct tatataatgt ggatgttggg cacagagctg tcatctttga	360
ctgattccag gacaaaaatg acaggacatt gtggtagggg actcactttc tcatccc atg ggt aca gaa acc aat tat ctt tgc ctt tct cca cca cgt aat gta Met Gly Thr Glu Thr Asn Tyr Leu Cys Leu Ser Pro Pro Arg Asn Val  1 5 10 15	417 465

cca atc Pro Ile	Ile Th													513
cgc atc Arg Ile														561
agc atc Ser Ile 50	gga ga Gly Gl	ag gac lu Asp	tat Tyr	gat Asp 55	gag Glu	cct Pro	gtg Val	ctg Leu	acg Thr 60	tac Tyr	atc Ile	acg Thr	acc Thr	609
gag atc Glu Ile 65														657
act cag Thr Gln														705
caa gca Gln Ala	Ala Th													753
ctg acc Leu Thr	ttt gg Phe Gl 115	ga aag ly Lys	gag Glu	ttc Phe	aca Thr 120	gaa Glu	gca Ala	gtg Val	gaa Glu	gcc Ala 125	aaa Lys	cag Gln	gtg Val	801
gct cag Ala Gln 130	cag ga	aa gca lu Ala	gag Glu	agg Arg 135	gcc Ala	aga Arg	ttt Phe	gtg Val	aag Lys 140	gaa Glu	aag Lys	gct Ala	gag Glu	849
cag cag Gln Gln 145														897
gca gcc Ala Ala														945
gcc aac Ala Asn	Ser Le													993
ttg gaa Leu Glu							tga *	c ct	cacct	gccg	g gcg	gggg	cagt	1044
ccgctcct	tcc ggd	ctgccc	ca to	gaggg	gccca	a ccc	ctgco	ctgc	acct	ccg	cag g	gctga	actggg	1104
ccacagco	ccc aat	tgattc	tt aa	acact	gcct	t tac	cccc	ccta	ccc	cagaa	aat d	cacto	gaaatt	1164
tcataatt	tgg ctt	taaagt	ga ag	ggaaa	ataaa	a agt	caaaa	atca	ctto	cagaa	act o	cttaa	aaaaaa	1224
aaaaa														1229

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gcc ttt cat agc act gcc ttg gat aag gaa att aca tca gca aat tat Ala Phe His Ser Thr Ala Leu Asp Lys Glu Ile Thr Ser Ala Asn Tyr 10 15 20	159
gct ggt gtc tgt aca tca tct gtg att aaa gaa gaa aac att gat caa Ala Gly Val Cys Thr Ser Ser Val Ile Lys Glu Glu Asn Ile Asp Gln 25 30 35 40	207
cca gga tac tgt tat ctc tca cct gat gga aag aga aaa act atg ctc Pro Gly Tyr Cys Tyr Leu Ser Pro Asp Gly Lys Arg Lys Thr Met Leu 45 50 55	255
tgc ttg gct tgt gga caa tcc atg aga aca gag aaa gga ctg aaa caa Cys Leu Ala Cys Gly Gln Ser Met Arg Thr Glu Lys Gly Leu Lys Gln 60 65 70	303
ttg ctt cca ggg gtt cca ttc ctc tgt att tca ggc acc aag act cag Leu Leu Pro Gly Val Pro Phe Leu Cys Ile Ser Gly Thr Lys Thr Gln 75 80 85	351
aag ccc ttc tta caa ggg ccc ttc aag gtc atc agt gtg gct gag gtt Lys Pro Phe Leu Gln Gly Pro Phe Lys Val Ile Ser Val Ala Glu Val 90 95 100	399
gat ttg tcg tgt gac aag gct gaa aaa act cta agt tac tac caa gca Asp Leu Ser Cys Asp Lys Ala Glu Lys Thr Leu Ser Tyr Tyr Gln Ala 105 110 115 120	447
cgt cta ttg tct tta cgg atg aag acc tgc acg caa gct gca tct cac Arg Leu Leu Ser Leu Arg Met Lys Thr Cys Thr Gln Ala Ala Ser His 125 130 135	495
agt ggc atg gca gcc aca cac cag aag gca gtg aaa ata att gca tac Ser Gly Met Ala Ala Thr His Gln Lys Ala Val Lys Ile Ile Ala Tyr 140 145 150	543
aaa aat ggg gat ggg tat cgt aat ggg aag tta att gtg gct gga aca Lys Asn Gly Asp Gly Tyr Arg Asn Gly Lys Leu Ile Val Ala Gly Thr	591

		155					160					165				
		Met			aca Thr	_	_	_	-					_	_	639
					tat Tyr 190											687
					tgg Trp										-	735
					caa Gln											783
	-	-	_	_	gaa Glu	_			_	_					_	831
		_			gtg Val			-	_	_	_			_	_	879
					atc Ile 270											927
					cta Leu											975
					tgg Trp											1023
			_		aaa Lys	_	_	-					_	_		1071
					acc Thr											1119
					ggc Gly 350											1167
					aga Arg											1215
					ata Ile											1263

1311 gtc aag ccg agc aac ctg tat aag cag ccc aac aca aaa cga gtg tgg Val Lys Pro Ser Asn Leu Tyr Lys Gln Pro Asn Thr Lys Arg Val Trp 405 395 400 att tat cta aat gga ggc aga cct gaa gat ggc act tat gcc tgg ggc 1359 Ile Tyr Leu Asn Gly Gly Arg Pro Glu Asp Gly Thr Tyr Ala Trp Gly 410 415 1407 aaa act att tca gag ctg ctg caa gac tgc tcc tct cgt ctc aaa atg Lys Thr Ile Ser Glu Leu Leu Gln Asp Cys Ser Ser Arg Leu Lys Met 430 acc cac cca gct aga gca ctg tac acc ccc agt gga gag cca att cag 1455 Thr His Pro Ala Arg Ala Leu Tyr Thr Pro Ser Gly Glu Pro Ile Gln 1503 tcc tgg gac gac ata gag cga gat atg gtc atc tgt gtg tct atg gga Ser Trp Asp Asp Ile Glu Arg Asp Met Val Ile Cys Val Ser Met Gly 460 465 cat ggt ttc aaa acc cca aaa gag tta aaa caa ctg atg gag atc aga 1551 His Gly Phe Lys Thr Pro Lys Glu Leu Lys Gln Leu Met Glu Ile Arg 475 480 485 1599 gca aat tat gcc aga atc cga agg cag cag ggc cct caa gcc aca gac Ala Asn Tyr Ala Arg Ile Arg Gln Gln Gly Pro Gln Ala Thr Asp 490 495 500 1647 att gtg gtg tca cca tcc acg aag ctg ctg tct ctg gca cat ctc cac Ile Val Val Ser Pro Ser Thr Lys Leu Leu Ser Leu Ala His Leu His 520 515 505 510 1703 aat taa ctcctatcag aaccatcgga ttttctgctg tatttttctg gaaagaaaac Asn \* 1763 tttctttacc cacttataaa cagaagactg tgacaagaag gccaattatt tccatcgctg aagactctaa atttggcaaa tcttctaaat aacaatcctg catagtttat taaaaaaaaat 1823 1883 tagtcgtaaa atttatcctt caaaaatctg cattttaaat aaaccctgac agtgatttct 1943 caagactgta aagatattag tctgagaatg caactctaac agactgctct gggcatcttt 2003 tctctttgcc ttggccaggc ctctcagaat tgagtgagcg tgtgactcca tttgcacagt 2063 gggacagata gtacaactga aataaaaagt ggaggcctct gcaaaaaata aaaaataaaa aataaattta tccttcaaaa taactcagtt ttttcaatgg gcctattttt aagaatgaac 2123 2173 attgaaaaat gagacaatat atccataaat tcatagtatg acataccata

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                                                                      120
                                                                      180
agctgtaaca tgttaatcag aactacctgg catcttcctg aacaagactt tcaatagggg
                                                                      227
         atg ctt cgc ttc atc cag aag ttt tct caa gca tct tca aag
ccagt
         Met Leu Arg Phe Ile Gln Lys Phe Ser Gln Ala Ser Ser Lys
                                                                      275
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Ile Leu Lys Tyr Ser Phe Pro Val Gly Leu Arg Thr Ser Arg Thr Asp
                                                                      323
ata ctt tct ctc aag atg tct ctc cag caa aac ttt tcc cca tgt cca
Ile Leu Ser Leu Lys Met Ser Leu Gln Gln Asn Phe Ser Pro Cys Pro
                 35
                                                                      371
agg cct tgg ctt tcc tca tca ttt cca gcg tat atg agc aag aca cag
Arg Pro Trp Leu Ser Ser Phe Pro Ala Tyr Met Ser Lys Thr Gln
             50
                                 55
                                                                      419
tgc tat cat aca tcc ccc tgc agc ttt aaa aag cag cag aag caa gca
Cys Tyr His Thr Ser Pro Cys Ser Phe Lys Lys Gln Gln Lys Gln Ala
                             70
         65
ctt cta gcc aga ccc tca agc acc atc act tac cta act gac agc cca
                                                                      467
Leu Leu Ala Arg Pro Ser Ser Thr Ile Thr Tyr Leu Thr Asp Ser Pro
                         85
     80
                                                                      515
aag cca gca tta tgt gta act ctg gca gga cta atc ccc ttc gtt gct
Lys Pro Ala Leu Cys Val Thr Leu Ala Gly Leu Ile Pro Phe Val Ala
                                                             110
                    100
95
                                                                      563
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Phe Thr Gln Met Ala Tyr Gly Ala Ser Phe Leu Ser Phe Leu Gly Gly
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Ile Arg Trp Gly Phe Ala Leu Pro Glu Gly Ser Pro Ala Lys Pro Asp 145 150 707 tac ctt aat tta gct agc agt gca gct cct ctt ttc ttt tca tgg ttt Tyr Leu Asn Leu Ala Ser Ser Ala Ala Pro Leu Phe Phe Ser Trp Phe 160 165 755 gcc ttc ctt att tct gaa aga ctt agt gaa gcc ata gtc aca gta ata Ala Phe Leu Ile Ser Glu Arg Leu Ser Glu Ala Ile Val Thr Val Ile 180 803 atg ggt atg gga gta gca ttc cac ctt gaa ctt ttt ctc tta cca cat Met Gly Met Gly Val Ala Phe His Leu Glu Leu Phe Leu Leu Pro His 195 200 tat ccc aac tgg ttt aaa gcc ctg agg ata gta gtc act tta ttg gcc 851 Tyr Pro Asn Trp Phe Lys Ala Leu Arg Ile Val Val Thr Leu Leu Ala 215 210 899 act ttt tca ttt ata atc act tta gta gtt aaa agt agt ttt cca gaa Thr Phe Ser Phe Ile Ile Thr Leu Val Val Lys Ser Ser Phe Pro Glu 225 230 950 aaa qqa cat aag aga cct ggt caa gta taa a aaatataaaa gtctgggaag Lys Gly His Lys Arg Pro Gly Gln Val 240 245 tgaggagcac ctctgcccag ctgctgcccc gtctgggaag tgaggagcgc ctctgcctgg 1010 1070 ccgcctgacc atctgggaag tgtgacaagc gcctctgccc ggccgctgtg caaccttcca cgtgtgaagt gacagccttg tgtgtgatct tttctgtctt ccccaagttt gcattttcga 1130 1190 cattaaagtt tactttttag ttaaaagttt aaaaaatata tataaataca ctgtagagan aacatgtgtn tgccagctac acctttctcn acttctgttt ggcttttttt ccccacacca 1250 atggtaattt atcttcacag atngttcttc atttctagaa attgttactt catggtaatt 1310 acttgagcaa aagcttgaaa atccctgaca agtacttntc atctcatagt atattagttt 1370 tcactcagtc attttatgaa taatanagtt atccacttaa acatttcaat aatgtaacca 1430 1432

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<sup>&</sup>lt;211> 2047

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<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (269)..(1372)

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agt gcg tat cac gct tcc cgc aag gac atg ctg gat gcc ttg ggc ata Ser Ala Tyr His Ala Ser Arg Lys Asp Met Leu Asp Ala Leu Gly Ile 185 190 195 200	868
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cac tac cag tac aag agc atc cct gtg gag gac aac cac aag gca gac His Tyr Gln Tyr Lys Ser Ile Pro Val Glu Asp Asn His Lys Ala Asp 220 225 230	964
atc agc tcc tgg ttc aac gag gcc att gac ttc ata gac tcc atc aag  Ile Ser Ser Trp Phe Asn Glu Ala Ile Asp Phe Ile Asp Ser Ile Lys  235 240 245	1012
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Pro Glu Cys His Thr Lys Glu Gln Ile Leu Asp Leu Leu Val Leu Glu

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gag Glu 120	aga Arg	gag Glu	ctt Leu	gat Asp	gaa Glu 125	cct Pro	gga Gly	aag Lys	cag Gln	gtc Val 130	cca Pro	ggc Gly	aat Asn	tca Ser	gaa Glu 135	675
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	120
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-	-					caa Gln									_		535
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						att Ile											631
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						gcc Ala				-	-						727
						agt Ser											775
						cgt Arg											823
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C						cag Gln 200											919
	_	_				aaa Lys	_						_				967
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I						aca Thr 280											1159
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cag cat ctg tca ac Gln His Leu Ser Th 645	a tcc tta atg cag r Ser Leu Met Gln 650	atg cta ctg gac agt Met Leu Leu Asp Ser 655	gag tta 2263 Glu Leu
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gct tct aag tac ct Ala Ser Lys Tyr Le 725	t cgg gtg aat cca u Arg Val Asn Pro 730	aac aca gcc ctt act Asn Thr Ala Leu Thr 735	ctt ttg 2503 Leu Leu
		aac aat ata ttt gct Asn Asn Ile Phe Ala 750	

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<sup>&</sup>lt;211> 591

<sup>&</sup>lt;212> DNA

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Met Tyr Ser Gly Ala Gly Pro Ala

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								acc Thr								269
								atc Ile								317
								aag Lys 65								365
								cac His								413
								agg Arg								461
								gtg Val								509
								aag Lys								557
								gat Asp 145								605
								gcc Ala								653
								gtg Val								701
								ggc Gly								749
								tct Ser								797
att Ile	gat	ata	tca	qca	aca	gcg	ttt	tac	aag	gca	cag	cca	gta	atc	gag	845

	_	_	-	_	_	gat Asp			-		_	_				893
	_		-			agg Arg 255	_	_				-				941
						cac His										989
_	_					cgg Arg		_	-							1037
_	-		-		_	acg Thr			-	_		-				1085
_	-			_	_	gtt Val	_	-						-		1133
	_		_		_	aaa Lys 335						-		-		1181
			_			aga Arg	-									1229
			-		_	gcg Ala		-		_			-			1277
_			_		_	atg Met	_		_	_						1325
	-	-	-			atc Ile										1373
						ccg Pro 415										1421
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					act Thr											2333
					acg Thr											2381
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	_			-	agg Arg			_		-	_	_		_	-	2621
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					gtc Val											2717
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caaa	cttg	gga t	tttç	gaact	g ca	agaco	tgta	a tga	agaac	cca	atgt	cata	agg a	aata	atggtt	2952
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Ile	Lys 120	Tyr	Ser	Cys	Pro	Lys 125	Gly	Tyr	Arg	Leu	Ile 130	Gly	Ser	Ser	Ser	
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	cgtc	cgg a	aagga												eggtgg egeega	60 120
tagg	ggga	ggg a	aagga	gctgt	it ta	agago	ccacç	g agt	taco	cgga	gcg	cctga	att (	cctgo		
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		gag Glu														704
		gat Asp 180														752
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		ctg Leu														944
		aaa Lys 260														992
		tgc Cys														1040
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att cca aaa gca Ile Pro Lys Ala 340	Lys Ser Thr	-		<u> </u>
act tct gct gct Thr Ser Ala Ala 355		-		_
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caa aag cta aag Gln Lys Leu Lys .				
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aat agg gga ctt . Asn Arg Gly Leu ' 420	Thr Pro Arg A			
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cag gtt cgt gaa g Gln Val Arg Glu V 450		Glu Glu Gln A		-
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aaaaaaaa				1685

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<sup>&</sup>lt;213> Homo sapiens

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cgaggactaa atgtgggtgc ccgagcttgg gacaagggag aggtcttg atg ttt ttc Met Phe 1	297
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tta aat gct gag cca ggt aag aag gtg ttt tac cct gtg gtg ttc agt Leu Asn Ala Glu Pro Gly Lys Lys Val Phe Tyr Pro Val Val Phe Ser 20 25 30 35	393
ctt tac aat cct gcc att gtt tat gcc aac cag gaa gtg cca cca cct Leu Tyr Asn Pro Ala Ile Val Tyr Ala Asn Gln Glu Val Pro Pro 40 45 50	441
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ctt tat cga aaa tac tta cat ggt gac ctc att gtg att cgg act ccg Leu Tyr Arg Lys Tyr Leu His Gly Asp Leu Ile Val Ile Arg Thr Pro 100 105 110 115	633
gtt cct ggt ctt ttc cac ctc tgg cat gaa aag cgc tgt gct gat gag Val Pro Gly Leu Phe His Leu Trp His Glu Lys Arg Cys Ala Asp Glu 120 125 130	681
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Glu	Thr 165	His	Leu	His	Lys	Gln 170	Ala	Tyr	Arg		175	Ser	GIU	Ala	vai	
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881

Gly 180 941 tagccttact tctacttcca gatgcagtgc ctcttttgga gaagacatgt ttattttca 1001 tgttctttct gacattactt tagcaattca acttgatgtg agaagaaaaa acaaatgttt 1061 caacacaaaa tctctgtttt gtgagaatac tgcactatgg aataattgac aaattgaaat 1121 ctcatatttg tcccaaaagt tgttttgagt tagttctacc tggtgcccat gttctgattg 1181 tgtgtgggat tgcatggtgt cctgattgca tctaggtgga gcggatggaa tgtgctgggc 1241 cactgttggg tggagagcag cacattctta cagaggagat ggagcgttat gagcatagta tgtggatagg tatcttcacc tgcccgcccc tgagtcagcc tccttgactt gatagcttga 1301 1361 agaatccttt tccactgaaa tagaggataa ttaattgaca catctgaaat ccccaatcaa tcaatcaaga gaaaggtaga actaaaaact ccttaactta ctgttgctta cacccctgaa 1421 1481 agtctgtttt taagcaaatg ggtaatagta gaaaataggt tagaatctat ggcttgatta aaaatatgtt attacattat catgttcagg attaggatta gtagtcagtt gctgtaaact 1541 1601 attttgaaca aacagaaaag aacacggaaa catttttaac agagcattta attatgttgg aatacaggat cctagctctg tctgggaaca ttagtttatg tgagccagct ctatcagggt 1661 cttcccatgg tggttcagaa tagatgagca tagcatggtt ttgtttgttt ttgctttcaa 1721 1781 ttttctaatt tggcatggat ccatatgtat ttactatcct ttttctaata tattaatata 1841 tgctacattt gtatttgcat tactataata ctttgagttg aaaaagagtt tcattgtgga 1901 gagaaaaagc aaatggtatg ccacaagatc actctgattt gagaaaaggg aggaggggaa 1961 gatagtetga atggaaatet gaaataegga atgttttaga gaaatatgte aettgeatat 2021 agaatgtttt aattgaggta taaattaatg agacaaagtg aaaaagaaat tatattcaga 2081 taggactgca ctacattatt tgtcacacat ggatctgtta ccatcaggtc aattcctagt atgcataaat tttttaaccc ttttaaaaga gacctatgtt gaaaacccct gaaaattcac 2141 2201 tgaagaaaaa tcattactct ttttctcagt aaatcatatc atctgaaata ttacaaattt caaatttcta ggtgctatat taattcaata ttacaataac tcttacctaa ttattcttac 2261 2321 aagttttaag ttgtggtagt ttagtgattt ttttaaaaaga tgtgtgaaat gttctctgca aaataattca ggccactgtc tccttttata tattattata attatttatt atgaagacca 2381

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135

436

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Leu Glu Ser Val Leu Glu Glu Glu Val Asp Asp Phe Pro Thr Phe Gly

130

125

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						aac Asn										580
-			_			gac Asp		-				_				628
-	-	_	_	_	_	ttc Phe		_		-	_		_		_	676
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	_		-	-	_	agc Ser		_		_	_		_			820
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						gcc Ala 305										964
	_		_	_	_	aaa Lys	_		_		-	_	_	_	_	1012
						aag Lys										1060
						gaa Glu										1108
gaa	aat	cca	tta	gat	gac	aat	tct	gag	gaa	gaa	atg	gaa	gat	gca	cca	1156

Glu Asn Pro Leu Asp Asp Asn Ser Glu Glu Glu Met Glu Asp 365 370 375	o Ala Pro	
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<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (23)..(1618)

<sup>&</sup>lt;400> 56

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cgg Arg	cgc Arg	gac Asp	gcc Ala	agc Ser 15	gag Glu	gag Glu	gag Glu	ctc Leu	aag Lys 20	aag Lys	gcc Ala	tat Tyr	cgg Arg	aag Lys 25	ctg Leu	100
gcc Ala	ctg Leu	aaa Lys	tgg Trp 30	cac His	ccg Pro	gat Asp	aaa Lys	aat Asn 35	ctg Leu	gat Asp	aat Asn	gcc Ala	gca Ala 40	gaa Glu	gca Ala	148
								gca Ala								196
cct Pro	cag Gln 60	gaa Glu	aga Arg	gca Ala	tgg Trp	tat Tyr 65	gat Asp	aat Asn	cat His	aga Arg	gag Glu 70	gcc Ala	cta Leu	ctt Leu	aaa Lys	244
ggt Gly 75	ggg Gly	ttt Phe	gat Asp	ggc Gly	gaa Glu 80	tat Tyr	caa Gln	gat Asp	gac Asp	agc Ser 85	tta Leu	gat Asp	ttg Leu	cta Leu	cgc Arg 90	292
								ggt Gly								340
								ttt Phe 115								388
								gtt Val								436
gac Asp	tcc Ser 140	cag Gln	agt Ser	gac Asp	tat Tyr	gat Asp 145	acg Thr	gta Val	gtc Val	cat His	cct Pro 150	ttc Phe	tac Tyr	gct Ala	tat Tyr	484
								aat Asn								532
gat Asp	aca Thr	cga Arg	cag Gln	gct Ala 175	tca Ser	aac Asn	cgc Arg	tgg Trp	gaa Glu 180	aaa Lys	cga Arg	gcc Ala	atg Met	gaa Glu 185	aaa Lys	580
gaa Glu	aac Asn	aaa Lys	aag Lys 190	att Ile	cgg Arg	gac Asp	aaa Lys	gca Ala 195	agg Arg	aaa Lys	gag Glu	aag Lys	aat Asn 200	gag Glu	ctt Leu	628
gtc Val	cgt Arg	cag Gln 205	ctg Leu	gta Val	gct Ala	ttc Phe	att Ile 210	cgt Arg	aaa Lys	aga Arg	gat Asp	aaa Lys 215	aga Arg	gtg Val	cag Gln	676
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gag Glu	ctc Leu	cag Gln	gag Glu 270	atg Met	gag Glu	gca Ala	cgg Arg	tac Tyr 275	gag Glu	aag Lys	gag Glu	ttt Phe	gga Gly 280	gat Asp	gga Gly	868
tcg Ser	gat Asp	gaa Glu 285	aat Asn	gaa Glu	atg Met	gaa Glu	gaa Glu 290	cat His	gaa Glu	ctc Leu	aaa Lys	gat Asp 295	gag Glu	gag Glu	gat Asp	916
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tac Tyr 315	tgc Cys	cca Pro	gca Ala	tgt Cys	gac Asp 320	aaa Lys	tcg Ser	ttc Phe	aag Lys	aca Thr 325	gaa Glu	aag Lys	gcc Ala	atg Met	aag Lys 330	1012
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caa Gln	cag Gln	ctg Leu	gag Glu 350	gag Glu	gaa Glu	gaa Glu	gaa Glu	aat Asn 355	ttt Phe	tca Ser	aga Arg	cct Pro	caa Gln 360	att Ile	gat Asp	1108
gaa Glu	aat Asn	cca Pro 365	tta Leu	gat Asp	gac Asp	aat Asn	tct Ser 370	gag Glu	gaa Glu	gaa Glu	atg Met	gaa Glu 375	gat Asp	gca Ala	cca Pro	1156
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aag Lys	gtt Val	gat Asp	cca Pro	gaa Glu 415	gat Asp	act Thr	aac Asn	tta Leu	aat Asn 420	caa Gln	gac Asp	agt Ser	gcc Ala	aaa Lys 425	gaa Glu	1300
ttg Leu	gaa Glu	gat Asp	agt Ser 430	ccc Pro	cag Gln	gaa Glu	aat Asn	gtc Val 435	agt Ser	gtc Val	aca Thr	gag Glu	atc Ile 440	att Ile	aaa Lys	1348
cca Pro	tgt Cys	gat Asp 445	gat Asp	cca Pro	aaa Lys	agt Ser	gaa Glu 450	gct Ala	aaa Lys	agt Ser	gtt Val	cct Pro 455	aaa Lys	ccc Pro	aaa Lys	1396

gga aag aaa acc aaa gat atg aaa aaa cct gtc aga gta cct gct gaa Gly Lys Lys Thr Lys Asp Met Lys Lys Pro Val Arg Val Pro Ala Glu 460 465 470	1444
CCa Caa aca atg agt gtt ctt atc agc tgt aca acc tgc cat agt gaaPro Gln Thr Met Ser Val Leu Ile Ser Cys Thr Thr Cys His Ser Glu475480	1492
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gca aga gca cct tca tca tcg tct tta aac agc gca aca agt agt caa Ala Arg Ala Pro Ser Ser Ser Ser Leu Asn Ser Ala Thr Ser Ser Gln 510 515 520	1588
agc aag aaa gag aaa cgt aaa aac aga tag a gattctgcct gtgcttttgt Ser Lys Lys Glu Lys Arg Lys Asn Arg * 525 530	1639
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gag Glu															149
ggc Gly															197
cgt Arg															245
agg Arg															293
ttc Phe 90			_		_	_		-							341
tcg Ser															389
cag Gln		_		_		_									437
cgc Arg	Gly	Ala	Gly	Glu	Gly	Gly	Pro	Tyr	Gly	Cys	Lys		Ala		485
cag Gln															533
ttc Phe 170															581
cag ( Gln (		-	_					_	_	_	_				629

ttt Phe	ctg Leu	gat Asp	atg Met 205	tgc Cys	atg Met	gat Asp	ctg Leu	aaa Lys 210	gtt Val	cat His	cct Pro	gaa Glu	cag Gln 215	gaa Glu	aag Lys	677
						atc Ile										725
gga Gly	act Thr 235	aag Lys	att Ile	att Ile	ggg Gly	aag Lys 240	gtt Val	cac His	gaa Glu	aag Lys	ttc Phe 245	acg Thr	ttg Leu	att Ile	gat Asp	773
ggc Gly 250	atc Ile	cgc Arg	gtg Val	gca Ala	aca Thr 255	ggc Gly	tcc Ser	tac Tyr	agt Ser	ttt Phe 260	aca Thr	tgg Trp	acg Thr	gat Asp	ggc Gly 265	821
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						cga Arg										917
						cac His										965
						cag Gln 320										1013
						agg Arg										1061
ctg Leu	gac Asp	cca Pro	gag Glu	atg Met 350	ccc Pro	gca Ala	gag Glu	ggc Gly	aag Lys 355	gca Ala	gag Glu	cgc Arg	aag Lys	ccc Pro 360	cat His	1109
						gtt Val										1157
agg Arg	gac Asp	gag Glu 380	ctc Leu	cag Gln	agc Ser	aga Arg	aag Lys 385	gcc Ala	att Ile	gac Asp	gct Ala	gcc Ala 390	act Thr	caa Gln	aca Thr	1205
						cca Pro 400										1253
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acc	agg	ata	gca	agc	tct	caa	acc	acg	att	tgg	tcc	aga	tcg	acc	act	1349

Thr Arg Ile Ala Ser Ser Gln Thr Thr Ile Trp Ser Arg Ser Thr Thr 430 435 440	
act cag act gac atg gat gag aac att ctc ttt cct cga gga act caa Thr Gln Thr Asp Met Asp Glu Asn Ile Leu Phe Pro Arg Gly Thr Gln 445 450 455	1397
tct aca gaa ggg tca cca gtc tca aaa atg tct gta tcg aga tct tcc Ser Thr Glu Gly Ser Pro Val Ser Lys Met Ser Val Ser Arg Ser Ser 460 465 470	1445
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atc agg tcc cgg ctc aac cac atg ctg gct atg ctg tca agg aga aca  Ile Arg Ser Arg Leu Asn His Met Leu Ala Met Leu Ser Arg Arg Thr  540 545 550	1685
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cctttgttgt ctttgaattc tttaggctgc atattatttt acatgctttg ttttgtcatg	1958
tatataccag gtattggttt tatggtttaa acactatgga tacaggggtt tgttttgcac	2018
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i L	aatgaaacga cccaggacat cgtttctggc tgcatcatta ttttgtgtcg cgtagtacca	a 240
= = 4	gatgggcagt cagtgagcgg cgcagggatg tgaacggacg gttttataat gtgaaaatti	300
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Ā	ctttattccc cctctgtctg caatatcagt gaactcaact ttgcagtgag gtggccaaaa	a 420
i t	agagagagaa tgaggagatc ttgatcatct tagtgtcaga ggagtcgcag cggactggga	a 480
i.	actgcagctg cgaccccccg cgtcctgtgc ggatttcagg gctgataccg cataggcggt	540
այում անագի անույ իրա	tatggaaagg acggtacacc ggagcggcgg aggatagaga ccctggcccc cggagaggtc	: 600
å	tgctgattte gcagcageet tegaageegt ggetgeettt catetgetge gttttattae	: 660
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	aga gac atc gag ctg aag ctg ggg cgc aaa gta ccc gag agt cta gtg Arg Asp Ile Glu Leu Lys Leu Gly Arg Lys Val Pro Glu Ser Leu Val 10 15 20 25	759
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				gag Glu												999	•
				ctc Leu 110												1047	•
ctt Leu	gta Val	atc Ile	aat Asn 125	gag Glu	agc Ser	atc Ile	gag Glu	tcc Ser 130	atc Ile	aag Lys	tgg Trp	atg Met	atc Ile 135	gaa Glu	gaa Glu	1095	
aaa Lys	gcc Ala	acc Thr 140	att Ile	acc Thr	agc Ser	aga Arg	ggc Gly 145	agc Ser	agc Ser	ctc Leu	agt Ser	ggc Gly 150	agc Ser	ctg Leu	tgc Cys	1143	
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ttg Leu	gac Asp	Gln	ttc Phe 205	agt Ser	gac Asp	agc Ser	tcc Ser	ctc Leu 210	ata Ile	gag Glu	gac Asp	tca Ser	cag Gln 215	gca Ala	cta Leu	1335	
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	_		_	_	tgg Trp			_				_				646
-	_		_		atg Met		-	_		_	_		_	_		694
-	_	_		~ -	ctg Leu	_	-	-	-		_			_		742
		~		_	ctg Leu 215		_				_			_		790
					ctg Leu											838
_				-	caa Gln	_			-	-			_			886
			_	_	tac Tyr	-		-		_	_		_	-		934
-	_	-	_		gaa Glu											982
	-		_		aag Lys 295	-				-	-		-	-	_	1030
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	_		~	_	_	aat Asn		~		_		_	_			2844
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tta cca gat ( Leu Pro Asp			lu Asn Asn		-	850
gaa tct aat a Glu Ser Asn 175						898
cag gac cat Gln Asp His ( 190	_				3	946
aag gtg cgt Lys Val Arg 205					•	994

							gat Asp									2042
							gtc Val									2090
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agg Arg	ttc Phe 270	gga Gly	cat His	cta Leu	gca Ala	cta Leu 275	atg Met	ttt Phe	ccc Pro	atg Met	ccc Pro 280	tct Ser	gcc Ala	tct Ser	gca Ala	2186
							cag Gln									2234
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tcc Ser	tgt Cys	tcc Ser	aag Lys 320	tca Ser	aga Arg	cca Pro	cat His	tta Leu 325	gct Ala	ggg ggg	aca Thr	cat His	act Thr 330	tct Ser	ctt Leu	2330
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							gta Val									2426
							cct Pro									2474
agt Ser	aat Asn	cgc Arg	atg Met	gtg Val 385	gtg Val	gaa Glu	agg Arg	agg Arg	tct Ser 390	caa Gln	tct Ser	gag Glu	atg Met	tta Leu 395	aat Asn	2522
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ctg	act	acc	tta	att	ggc	gct	gga	atc	cga	att	ctt	ttc	agt	tcc	tgc	2714

Leu Thr Thr Leu Ile Gly Ala Gly Ile Arg Ile Leu Phe Ser Ser Cys 445 450 450 460	
caa gaa gaa acc gca gat ttg cta aag gaa ctg tct tta gtg gaa caa Gln Glu Glu Thr Ala Asp Leu Leu Lys Glu Leu Ser Leu Val Glu Gln 465 470 475	2762
aga aag aat gtt ggt att cat gtt cca aca gtg gtg aat agt aat aaa Arg Lys Asn Val Gly Ile His Val Pro Thr Val Val Asn Ser Asn Lys 480 485 490	2810
agt gag gca ctc cag ttt tat tta agt att ccc aat ata agt tat ata Ser Glu Ala Leu Gln Phe Tyr Leu Ser Ile Pro Asn Ile Ser Tyr Ile 495 500 505	2858
act gca tta aat atg tgt cac cag ttt tca tct gtg aaa agg atg gct Thr Ala Leu Asn Met Cys His Gln Phe Ser Ser Val Lys Arg Met Ala 510 520	2906
aac agg tat gtc tgt tgt aat att ttt aaa tga ttactttt aaaagattcg Asn Arg Tyr Val Cys Cys Asn Ile Phe Lys * 525 530 535	2957
taaaagcatt ccatagaagt ttaatgttaa aaaaatttaa gcggcatcat gcctgttaga	3017
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agctgtagag gtgaagtaag cctgtgaagg accagc atg gga atc cta tac tct Met Gly Ile Leu Tyr Ser 1 5	354
gag ccc atc tgc caa gca gcc tat cag aat gac ttt gga caa gtg tgg	402

Glu Pro Ile Cys Gln Ala Ala Tyr Gln Asn Asp Phe Gly Gln Val Trp 10 15 20	
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aat gga gac acg ccc ctg atc tgt gct tgc agg cga ggg cat gtg aga Asn Gly Asp Thr Pro Leu Ile Cys Ala Cys Arg Arg Gly His Val Arg 40 45 50	498
atc gtt tcc ttc ctt tta aga aga aat gct aat gtc aac ctc aaa aac Ile Val Ser Phe Leu Leu Arg Arg Asn Ala Asn Val Asn Leu Lys Asn 55 60 65 70	546
cag aaa gag aga acc tgc ttg cat tat gct gtg aag aaa aaa ttt acc Gln Lys Glu Arg Thr Cys Leu His Tyr Ala Val Lys Lys Lys Phe Thr 75 80 85	594
ttc att gat tat cta cta att atc ctc tta atg cct gtt ctg ctt att Phe Ile Asp Tyr Leu Leu Ile Ile Leu Leu Met Pro Val Leu Leu Ile 90 95 100	642
ggg tat ttc ctc atg gta tca aag aca aag cag aat gag gct ctt gta Gly Tyr Phe Leu Met Val Ser Lys Thr Lys Gln Asn Glu Ala Leu Val 105 110 115	690
cga atg cta ctt gat gct ggc gtc gaa gtt aat gct aca gat tgt tat Arg Met Leu Leu Asp Ala Gly Val Glu Val Asn Ala Thr Asp Cys Tyr 120 125 130	738
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gcaaattact taatctcagt aggcctcagt tctctctttc accaaatcag gagaattatt	180									
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1 5										
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cta aga tat aca cac atg aag act gct ggt ggt gca agg tgt gga gtc Leu Arg Tyr Thr His Met Lys Thr Ala Gly Gly Ala Arg Cys Gly Val 25 30 35 40	328									
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aag gga ctt tgc tgt ggg ctg aag tga ccagg aagggctccg tggaggaagt Lys Gly Leu Cys Cys Gly Leu Lys * 60 65	428									
ggggcccaag gatggacagg acatggatgt ggcaggaaga gggagagcct taccagatgg	488									
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gat ggg ggc gac ggc cag gcc ggg ccc gac gag ggc gag gtg gac tcc Asp Gly Gly Asp Gly Gln Ala Gly Pro Asp Glu Gly Glu Val Asp Ser 30 35 40	147									
tgc ctg cgg caa gga aac atg aca gct gcc cta cag gca gct ctg aag Cys Leu Arg Gln Gly Asn Met Thr Ala Ala Leu Gln Ala Ala Leu Lys 45 50 55 60	195									
aac ccc cct atc aac acc aag agt cag gca gtg aag gtg agt cgc aga Asn Pro Pro Ile Asn Thr Lys Ser Gln Ala Val Lys Val Ser Arg Arg 65 70 75	243									
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agg aag cat gtg gtg aag gag gtg cta ggg gag cac ata gtg ccc tcc Arg Lys His Val Val Lys Glu Val Leu Gly Glu His Ile Val Pro Ser 10 15 20	160									
gac cag cag att gtc agg gta ctc agg acc cca ggg aac aat ctg Asp Gln Gln Gln Ile Val Arg Val Leu Arg Thr Pro Gly Asn Asn Leu 25 30 35	208									
cat gag gtg gag aca gcc caa ggg cag cgc ttc ctg gtg agc atg ccc His Glu Val Glu Thr Ala Gln Gly Gln Arg Phe Leu Val Ser Met Pro 40 45 50	256									
tcc aaa tac cgc aag aac atc tgg atc aag aga ggg gac ttt ctc att	304									

Ser Lys Tyr Arg Lys Asn Ile Trp Ile Lys Arg Gly Asp Phe Leu Ile 55 60 65 70	
gtt gac ccc att gaa gag gga gaa aag gtg aag gct gaa atc tcg ttt Val Asp Pro Ile Glu Glu Gly Glu Lys Val Lys Ala Glu Ile Ser Phe 75 80 85	352
gtg ctc tgc aag gac cac gtg cgc tct ctg cag aag gag ggg ttt tgg Val Leu Cys Lys Asp His Val Arg Ser Leu Gln Lys Glu Gly Phe Trp 90 95 100	400
cct gag gcc ttc tct gaa gtg gct gag aaa cac aac aac agg aac aga Pro Glu Ala Phe Ser Glu Val Ala Glu Lys His Asn Asn Arg Asn Arg 105 110 115	448
caa act caa cca gaa ctc cca gct gag cca cag tta tca gga gag gag Gln Thr Gln Pro Glu Leu Pro Ala Glu Pro Gln Leu Ser Gly Glu Glu 120 125 130	496
tcc agc tca gaa gat gat tct gac ctg ttt gtt aac aca aac cgc aga Ser Ser Ser Glu Asp Asp Ser Asp Leu Phe Val Asn Thr Asn Arg Arg 135 140 145 150	544
cag tat cat gag agt gag gag gag agt gaa gag gag g	592
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ctg gtg ggc tcg ccg cct tgg aaa gag gct ttc cgg cag aga tgc ctg Leu Val Gly Ser Pro Pro Trp Lys Glu Ala Phe Arg Gln Arg Cys Leu 15 20 25 30	155
gag aga atg aga aac agc cgg gac agg ctc cta aac agg tac cgc cag	203

Glu	Arg	Met	Arg	Asn 35	Ser	Arg	Asp	Arg	Leu 40	Leu	Asn	Arg	Tyr	Arg 45	Gln	
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														aat Asn		299
														gtg Val		347
														atc Ile		395
				-	_	_		-	-	_	_		_	atc Ile 125	_	443
														aca Thr		491
														ggc Gly		539
														cgt Arg		587
														cac His		635
														ctt Leu 205		683
						gat Asp			-				tag * 220	agcc	:agc	732
tggg	acto	ac a	tcat	tcta	ıt gg	gcgt	tgaa	gac	aact	cat	tcct	ctga	ıgg a	gcct	tgtac	792
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aaaaa											857					

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cgc	tggg.	acg	tatg	tgcc	ga g	ggcc	gcgg	c gt	ctga	cctc	atg	gcgt	aga	gcct	agcaac	180
agc	gcag	gct	ccca	gccg	ag t	ccgt	Me				a Va				g atg g Met	233
											Ser				gcc Ala 25	281
														gtg Val 40		329
														cca Pro		377
												_		aca Thr		425
											_			ctc Leu		473
														cct Pro		521
														gaa Glu 120		569
														cca Pro		617
														gac Asp		665
gac Asp														acc Thr	_	713

	155					160					165					
			agg Arg								Ser					761
			tcc Ser													809
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															ctacc	240
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ctaa	ccaa	ga a	gata	aaaσ	a ao	tatc	tata	caa	gata	tta	atat	ataa	αa t	aaca	ttata	360

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<213> Homo sapiens

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20

Pro Ser Tyr Leu Lys Ile Thr Cys Gly Lys Arg Ser Lys Gln Ile Thr

ccc atc tac tat ccc tcc cgc ctc ccc cct gtc aaa aga aag ttc tca 1348 Pro Ile Tyr Tyr Pro Ser Arg Leu Pro Pro Val Lys Arg Lys Phe Ser 25 30 35 gtt tat gat gca aaa ctt aca att gtt cat tta tcc aca ttc tca ata 1396 Val Tyr Asp Ala Lys Leu Thr Ile Val His Leu Ser Thr Phe Ser Ile 45 1446 gag gat ttt cca cta tat tta agt atg gca gga taa ttac ccacctgttc Glu Asp Phe Pro Leu Tyr Leu Ser Met Ala Gly 60 ctcttttcag cttagaaaca taacggttca ttccttttat tgctagagaa tgtcattcct 1506 gaagatttta taaacaaagg caaatatgaa ggaaaatttg taattatgaa ataagtcctt 1566 tgtagtaaag aatatttccc aaatcataac agttctattt ggaatgatac ccacaactct 1626 acaagcatct tatccctcta caggaatgac taccttatta attaaaataa aaatttaaca 1686 aggatcaaaa taaaattctt tagcaataga ctcctgcaaa aataaaaact aaaactagac 1746 ctagtcattg ccatttgatc aaacttagaa caggcttaaa taacagaacc actccattaa 1806 agaggcatag aaagaaaagt ttactaaaat aaatgtaaaa gtcttatgga gatgaagatc 1866 tctagaatag tcttaagtct atgactactg ctatcattaa tgagcaaata aatgacttga 1926 aattattccn cctggaaaag gtaaactcat acgtattatg gaaaangcct atgggcactt 1986 agaaaaatat tcctgggtaa gtaaaccatg gnaaatatag ggtacatcct aagcctctcc 2046 2100 gccctaactt ttaaaattat tnttggagaa aggatagcac tagccgggga ggaa

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						gag Glu										4	137
						gtc Val										4	185
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	_					tac Tyr		_	_		-					5	581
						cgg Arg										6	529
_	-	_				gtc Val		_	_	-		~				6	577
-	_			_		gag Glu	_	-		_		_		-		7	25
_			_			gac Asp 160	_	_		~ ~	~		~		~ ~	7	73
	-	-			_	agc Ser	-		-	_					_	8	21
			_	_		acc Thr	_	-	-		_	_		tga * 200	ggc	8	69
tgga	cato	gg c	ccgc	tccc	c ac	aatg	aaat	aaa	igtta	ttt	tctc	atto	cc a	aaaa	ıaaaaa	9	29
aaaa	L															9	33

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ca: Gl:	g gat n As <u>r</u>	gco Ala	c cat a His 125	Gly	g cag / Glr	g cct n Pro	gat Asp	gto Val 130	l Ser	gco Ala	c tti a Phe	t gac e Asp	tto Phe 135	e Thi	g agc r Ser	856
atq Me1	g ato Met	g cgg : Arg 140	g Ala	ı gaç ı Glı	g agt ı Ser	tct Ser	gct Ala 145	. Arg	gtg Val	caa Glr	ı gaç ı Glı	g aag 1 Lys 150	His	ggo Gly	c gcc / Ala	904
cgo Arg	cto Leu 155	ı Leı	g ctg 1 Leu	gga Gly	ctg Leu	gtg Val 160	ggg	gac Asp	tgc Cys	ctg Leu	gtg Val 165	. Glu	cco Pro	tto Phe	tgg Trp	952
Pro 170	) Leu	ggc Gly	act Thr	gga Gly	gtg Val 175	Ala	cgg Arg	ggc	ttc Phe	ctg Leu 180	Ala	gcc Ala	ttt Phe	gat Asp	gca Ala 185	1000
gcc Ala	tgg Trp	atg Met	gtg Val	aag Lys 190	Arg	tgg Trp	gca Ala	gag Glu	ggc Gly 195	Ala	gag Glu	tcc Ser	cta Leu	gag Glu 200	gtg Val	1048
ttg Leu	gct Ala	gag Glu	cgt Arg 205	gag Glu	agc Ser	ctg Leu	tac Tyr	cag Gln 210	Leu	ctg Leu	tca Ser	cag Gln	aca Thr 215	tcc Ser	cca Pro	1096
gaa Glu	aac Asn	atg Met 220	His	cgc Arg	aat Asn	gtg Val	gcc Ala 225	cag Gln	tat Tyr	ggg Gly	ctg Leu	gac Asp 230	cca Pro	gcc Ala	acc Thr	1144
cgc Arg	tac Tyr 235	ccc Pro	aac Asn	ctg Leu	aac Asn	ctc Leu 240	cgg Arg	gca Ala	gtg Val	acc Thr	ccc Pro 245	aat Asn	cag Gln	gta Val	cga Arg	1192
gac Asp 250	ctg Leu	tat Tyr	gat Asp	gtg Val	cta Leu 255	gcc Ala	aag Lys	gag Glu	cct Pro	gtg Val 260	cag Gln	agg Arg	aac Asn	aac Asn	gac Asp 265	1240
aag Lys	aca Thr	gat Asp	aca Thr	ggg Gly 270	atg Met	cca Pro	gcc Ala	acc Thr	ggg Gly 275	tcg Ser	gca Ala	ggc Gly	acc Thr	cag Gln 280	gag Glu	1288
gag Glu	ctg Leu	cta Leu	cgc Arg 285	tgg Trp	tgc Cys	cag Gln	Glu	cag Gln 290	aca Thr	gct Ala	gly ggg	tac Tyr	ccg Pro 295	gga Gly	gtc Val	1336
cac His	gtc Val	tcc Ser 300	gat Asp	ttg Leu	tct Ser	tcc Ser	tcc Ser 305	tgg Trp	gct Ala	gat Asp	ggg Gly	cta Leu 310	gct Ala	ctg Leu	tgt Cys	1384
gcc Ala	ctg Leu 315	gtg Val	tac Tyr	cgg Arg	Leu	cag Gln 320	cct Pro	ggc Gly	ctg Leu	Leu	gaa Glu 325	ccc Pro	tca Ser	gag Glu	ctg Leu	1432
cag Gln 330	Gly ggg	ctg Leu	gga Gly	Ala	ctg Leu 335	gaa Glu .	gca Ala	act Thr	Ala	tgg Trp 340	gca Ala	cta Leu	aag Lys	gtg Val	gca Ala 345	1480
gag	aat	gag	ctg	ggc	atc	aca (	ccg	gtg	gtg	tct	gca	cag	gcc	gtg	gta	1528

Glu	. Asn	Glu	Leu	Gly 350		Thr	Pro	Val	Val 355		Ala	. Gln	Ala	Val 360		
			gac Asp 365						Ala					Phe		1576
								Ser							gcc Ala	1624
			acc Thr													1672
_			cga Arg													1720
			cgc Arg													1768
			cca Pro 445													1816
			ggt Gly													1864
			gaa Glu													1912
			tgc Cys													1960
			cca Pro													2008
cag Gln	aca Thr	gac Asp	cac His 525	aaa Lys	gag Glu	gaa Glu	ggc Gly	agc Ser 530	gat Asp	aga Arg	ggc Gly	cct Pro	gag Glu 535	agt Ser	ccg Pro	2056
gag Glu	ctc Leu	ccc Pro 540	aca Thr	cca Pro	agt Ser	gag Glu	aat Asn 545	agc Ser	atg Met	cca Pro	cca Pro	ggc Gly 550	ctc Leu	tca Ser	act Thr	2104
			tcg Ser													2152
ccc Pro	acc Thr	cgt Arg	cgg Arg	cag Gln	atc Ile	cgc Arg	ctc Leu	tcc Ser	agc Ser	ccg Pro	gag Glu	cgc Arg	cag Gln	cgg Arg	ttg Leu	2200

570				575			580			585	
tcc t Ser S											2248
cct c Pro E											2296
ttt g Phe V											2344
atg g Met G											2392
gaa g Glu A 650											2440
gcc a Ala I											2488
ctg c Leu I											2536
cag a Gln T	Thr			_							2584
cta g Leu G 7											2632
agt t Ser S 730		_	_		_		 	 _			2680
ctc g Leu V											2728
atc a Ile T											2776
cag g Gln G	3lu										2824
gct g Ala A 7											2872

gtc aac cag aga gat gcc ctc atc cgc ttc cag gag gag cgc agg ctc Val Asn Gln Arg Asp Ala Leu Ile Arg Phe Gln Glu Glu Arg Arg Leu 810 815 820 825	2920
agc gag ctg gcc ttg ggg aca ggg gcc cag ggc tag acga gggtgggccg Ser Glu Leu Ala Leu Gly Thr Gly Ala Gln Gly * 830 835	2970
tctgctttcg ttcccacaaa gaaagcacct caccccagca cagtgccacc cctgttcatc	3030
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	120
aaattgagag cgttttcgca ctccagcggc tgctcctggc ggctctgcgg ccgtcacc atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr 1 5 10	178 226
atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr	178
atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr  1 5 10 15  cgt ttg gat tac cat gag aaa aag aga aag gaa agt cga gag gct Arg Leu Asp Tyr His Glu Lys Lys Arg Lys Lys Glu Ser Arg Glu Ala	178 226
atg cca cag aat gaa tat att gaa tta cac cgt aaa cgc tat gga tac Met Pro Gln Asn Glu Tyr Ile Glu Leu His Arg Lys Arg Tyr Gly Tyr  1 5 10 15  cgt ttg gat tac cat gag aaa aag aga aag aag gaa agt cga gag gct Arg Leu Asp Tyr His Glu Lys Lys Arg Lys Lys Glu Ser Arg Glu Ala 20 25 30  cat gaa cgt tca aag aag gca aag aaa atg att ggt ctg aag gct aag His Glu Arg Ser Lys Lys Ala Lys Lys Met Ile Gly Leu Lys Ala Lys	178 226 274

aca cca cag gga gca gta cct gcc tat ctg ctg gac aga gag gga caa Thr Pro Gln Gly Ala Val Pro Ala Tyr Leu Leu Asp Arg Glu Gly Gln

tct Ser	cga Arg	gct Ala	aaa Lys 100	gta Val	ctt Leu	tcc Ser	aat Asn	atg Met 105	att Ile	aaa Lys	cag Gln	aaa Lys	aga Arg 110	aaa Lys	gag Glu	514
aag Lys	gcg Ala	gga Gly 115	aaa Lys	tgg Trp	gaa Glu	gtc Val	cct Pro 120	ctg Leu	cct Pro	aaa Lys	gta Val	cgt Arg 125	gcc Ala	cag Gln	gga Gly	562
														aag Lys		610
gca Ala 145	tgg Trp	aag Lys	aga Arg	atg Met	gtt Val 150	act Thr	aaa Lys	gtg Val	tgc Cys	ttt Phe 155	gtt Val	gga Gly	gat Asp	ggc Gly	ttt Phe 160	658
aca Thr	aga Arg	aaa Lys	cca Pro	cct Pro 165	aaa Lys	tat Tyr	gaa Glu	aga Arg	ttc Phe 170	atc Ile	agg Arg	cca Pro	atg Met	ggc Gly 175	ttg Leu	706
cgt Arg	ttc Phe	aag Lys	aaa Lys 180	gcc Ala	cat His	gta Val	aca Thr	cat His 185	cct Pro	gaa Glu	ctg Leu	aaa Lys	gcc Ala 190	acc Thr	ttt Phe	754
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aca Thr	act Thr 210	ttg Leu	ggt Gly	gtt Val	att Ile	acc Thr 215	aaa Lys	ggt Gly	act Thr	gtc Val	att Ile 220	gaa Glu	gta Val	aat Asn	gtg Val	850
agc Ser 225	gaa Glu	ttg Leu	ggc Gly	ctt Leu	gtg Val 230	aca Thr	caa Gln	gga Gly	ggc Gly	aaa Lys 235	gtt Val	att Ile	tgg Trp	gga Gly	aaa Lys 240	898
														aat Asn 255		946
		ctg Leu		tga *	cago	caatt	tc a	atata	ataat	tt a	tgaç	ggact	aca	acaco	caat	1001
tgaa	agaaa	act g	gccat	tact	g to	gatgt	ttct	gaa	atact	tacc	aaad	cagco	cat a	acato	gtctgc	1061
aato	gaaga	aga t	ttat	taaa	at to	gtaaa	acatt	aaa	agtgg	gaaa	aaaa	aaaa	aa			1110

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<220>

<sup>&</sup>lt;211> 1835

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

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	gtc tta gcc tgg Val Leu Ala Trp 30			
	act gaa atg act Thr Glu Met Thr 45			
	tgg ccc ctc tgg Trp Pro Leu Trp			
	aat gcc tta ttt Asn Ala Leu Phe 80			
	aca agt ctg gtt Thr Ser Leu Val 95	Val Ser Pro G		
	aca gct gtt gta Thr Ala Val Val 110			
	atc cct ccc gct Ile Pro Pro Ala 125			
	agt tat agc cct Ser Tyr Ser Pro			
	agc tgt atg act Ser Cys Met Thr 160			
	ggc agt ggt tct Gly Ser Gly Ser 175	Tyr Ser Pro G		
	tat aat aag ttg Tyr Asn Lys Leu 190			
tct ccg tac cct	acc act gtt gga	cca gtg gag a	gc agt gga ttg	aga 676

Ser	Pro	Tyr	Pro	Thr 205	Thr	Val	Gly	Pro	Val 210	Glu	Ser	Ser	Gly	Leu 215	Arg	
							acc Thr									724
							cga Arg 240									772
-							gtt Val									820
							ttc Phe									868
							aag Lys									916
							aaa Lys									964
							gca Ala 320									1012
	_						aca Thr							_		1060
							gtt Val									1108
							cca Pro									1156
							gcc Ala									1204
							tat Tyr 400									1252
							gaa Glu									1300
							ggc Gly									1348

425	430	435	440
	Asp Ser Ala Ile	atc atg cat gta ttt Ile Met His Val Phe 450	
		ccg aag tat ccc gac Pro Lys Tyr Pro Asp 470	_
		aca cca aat aaa cca Thr Pro Asn Lys Pro 485	_
		cag agt gct atc aac Gln Ser Ala Ile Asn 500	
		gta tac aac ctg cca Val Tyr Asn Leu Pro 515	
	His Thr Leu Leu	atg ttt ctc tac atc Met Phe Leu Tyr Ile 530	
		gtt aat ctt ggt cta Val Asn Leu Gly Leu 550	
gtg aat ata ttg tgg Val Asn Ile Leu Trp 555		tag c aagtcatata ttt *	aattctg 1735
acatttagac tatttcact	tg aaccagaagt cga	aactaaa catctctgag c	cactgactc 1795
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<210> 78 <211> 1029

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (428)..(817)

<400> 78

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aattgaagaa aaaaggccaa gttaaaatag gaaaacaaat ggttttcatt tggtggcagt 180

240 tgaaatcaaa gtatacatgt gtatacattc taatccgtca tctatcccat gtggcatttt 300 360 ttttcccctt tcttttctct cgctttgcct tcagcctttt tctttgcctt tggttcatcc 420 atattgggta ctgtccatgc tggtcggcgt gagcgtgagg tgtgggtgtt cgtttctcag 469 qtaaaac atg gct aaa agc tta cgg agt aag tgg aaa aga aag atg cgt Met Ala Lys Ser Leu Arg Ser Lys Trp Lys Arg Lys Met Arg 517 gct gaa aag aga aaa aag aat gcc cca aag gag gcc agc agg ctt aaa Ala Glu Lys Arg Lys Lys Asn Ala Pro Lys Glu Ala Ser Arg Leu Lys 20 15 565 agt att ctc aaa cta gac ggt gat gtt tta atg aaa gat gtt caa gag Ser Ile Leu Lys Leu Asp Gly Asp Val Leu Met Lys Asp Val Gln Glu 45 35 ata gca act gtg gtg gta ccc aaa ccc aaa cat tgc caa gag aaa atg 613 Ile Ala Thr Val Val Val Pro Lys Pro Lys His Cys Gln Glu Lys Met 50 661 caa tgt gag gta aaa gat gaa aaa gat gac atg aaa atg gag act gat Gln Cys Glu Val Lys Asp Glu Lys Asp Asp Met Lys Met Glu Thr Asp 70 709 att aag aga aac aaa aag act ctt cta gac cag cat gga cag tac cca Ile Lys Arg Asn Lys Lys Thr Leu Leu Asp Gln His Gly Gln Tyr Pro 757 ata ton ato aac caa ago caa aga aaa ago cto aag oca aag coa gag Ile Trp Met Asn Gln Arg Gln Arg Lys Arg Leu Lys Ala Lys Arg Glu 100 105 805 aaa aga aag ggg aaa agc aaa gca aaa gca gtg aaa gtg gca aag ggt Lys Arg Lys Gly Lys Ser Lys Ala Lys Ala Val Lys Val Ala Lys Gly 120 115 860 ttg qcc tgg tag act cttaaaacct tggaaaatgc cacatgggat agatgacgga Leu Ala Trp 130 920 ttaqaatqta tacacatqta tactttgatt tcaactgcca ccaaatgaaa accatttgtt ttcctatttt aacttggcct tttttcttca attcaaaccc agcataactc ctcaagtttg 980 ttttgggaac ttgaataaaa tattttcttt gatacaaaaa aaaaaaaaa 1029

<sup>&</sup>lt;210> 79

<sup>&</sup>lt;211> 5476

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

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<222> (188)..(5149)
<400> 79

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Met 175	Lys	Gly	Thr	Lys	Val 180	Lys	Thr	Pro	Glu	Met 185	Ile	Ile	Gln	Lys	Pro 190	
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	gga Gly															853
	cct Pro															901
	cta Leu 240															949
	acc Thr															997
	gca Ala															1045
	ggg															1093
	gtc Val															1141
	atg Met 320															1189
	gaa Glu															1237
att Ile	tca Ser	ggg Gly	ccc Pro	aag Lys 355	gtc Val	aat Asn	gtg Val	gaa Glu	gcc Ala 360	cca Pro	gat Asp	gtc Val	aac Asn	ttg Leu 365	gag Glu	1285
	ctg Leu															1333
	gtc Val															1381
aaa Lys	ggt Gly	aca Thr	aag Lys	gtg Val	aag Lys	gga Gly	gag Glu	tat Tyr	gat Asp	gta Val	act Thr	gta Val	cca Pro	aag Lys	ctg Leu	1429

405 410 400 1477 gaa gga gaa ctc aaa ggc cca aaa gtg gac att gat gcc cca gat gtg Glu Gly Glu Leu Lys Gly Pro Lys Val Asp Ile Asp Ala Pro Asp Val 415 420 1525 gat gtt cat ggc cca gac tgg cac ttg aag atg ccc aag atg aaa atg Asp Val His Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 440 435 1573 ccc aaa ttc agt gtg cca ggg ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Val Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 450 1621 gtg aac ctg ccc aag gct gat gtg gac att tcc ggg ccc aag ata gat Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Ile Asp 465 gtt act gct cct gat gtg agc att gag gaa cca gaa ggg aaa ttg aaa 1669 Val Thr Ala Pro Asp Val Ser Ile Glu Glu Pro Glu Gly Lys Leu Lys 480 485 1717 ggg ccc aag ttt aag atg cct gag atg aac atc aaa gtc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Val Pro Lys Ile 500 1765 tcc atg cct gat gtg gac tta cat ctg aaa ggc cct aac gta aag gga Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Asn Val Lys Gly 515 1813 qaa tat gat gtc aca atg cca aag gtt gaa agt gag att aaa gtt cct Glu Tyr Asp Val Thr Met Pro Lys Val Glu Ser Glu Ile Lys Val Pro 535 530 1861 gat gtt gaa ctt aaa agt gcc aaa atg gac att gat gtc cca gat gtg Asp Val Glu Leu Lys Ser Ala Lys Met Asp Ile Asp Val Pro Asp Val 550 545 1909 gag gtt caa ggc cca gac tgg cac ctg aag atg ccc aag atg aaa atg Glu Val Gln Gly Pro Asp Trp His Leu Lys Met Pro Lys Met Lys Met 560 565 1957 ccc aag ttc agc atg cct ggc ttc aaa gca gag ggc cca gaa gtg gat Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro Glu Val Asp 575 580 590 gtg aac ctg ccc aag gct gat gtg gac atc tca gga ccc aag gtg ggt 2005 Val Asn Leu Pro Lys Ala Asp Val Asp Ile Ser Gly Pro Lys Val Gly 605 595 gtt gaa gtt cca gat gtg aat att gaa gga cct gaa gga aag ctg aag 2053 Val Glu Val Pro Asp Val Asn Ile Glu Gly Pro Glu Gly Lys Leu Lys 610 620 ggc ccc aag ttc aag atg cca gag atg aat atc aag gcc ccc aag atc 2101 Gly Pro Lys Phe Lys Met Pro Glu Met Asn Ile Lys Ala Pro Lys Ile 630 625

	_		_		_	_		_			cct Pro 650		_		_	2	2149
											gac Asp					2	2197
	-	_									cag Gln					2	2245
	_	_	_		_			-			ttt Phe	_	-			2	2293
											ctg Leu					2	2341
	-			_			_	_			gct Ala 730		-			2	2389
	_			-		_	_			-	aag Lys		_	-		2	2437
	-			_	_		_	-		_	cca Pro	_	-	-		2	2485
_						_				-	gat Asp			_		2	2533
_				_	_	_	-		-		gac Asp		-			2	2581
	-										caa Gln 810					2	2629
_	_				_	_		_		_	ttc Phe	_	_			2	2677
											ttg Leu					2	2725
		_									gcc Ala					2	2773

	gaa Glu			-		_	_	_			_		_			2821
	atg Met 880			_			-			_		-		_		2869
	ttg Leu					-			-	-						2917
	gta Val															2965
	atg Met															3013
	ctg Leu														_	3061
	aaa Lys 960															3109
	gat Asp	_				_		_	-	_	_		_		-	3157
	gag Glu							Lys					Lys			3205
	atg Met	His		_	_		Lys			_		Asp		_	_	3253
	ctt Leu 1	_				Leu					Asp					3301
Glu	gta Val 1040				Met					Val						3349
	gtt Val	_		Ser	_		-		Asp					Asp		3397
	ctg Leu	_	Met		_	-		Met		-		_	Met			3445
ttc	aaa	gga	gag	ggc	cct	gaa	gtg	gat	gtg	aag	ctg	ccc	aaa	gct	gac	3493

Phe	Lys	_	Glu 1090	Gly	Pro	Glu		Asp 1095	Val	Lys	Leu		Lys L100	Ala	Asp	
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Ile					Ala					Pro				atg Met		3589
				Lys					Ser					ggt Gly		3637
			Gly					Gly					Thr	gtt Val 1165		3685
		Glu					Ala					Ile		ggc Gly		3733
	Val					Pro					His			gac Asp		3781
His					Lys					Lys				cct Pro		3829
				${\tt Gly}$					Met					gct Ala		3877
			Ser					Asp					Asp	gtg Val 1245		3925
		Ala					Leu					Phe		atg Met		3973
-	Met			_	_	His					Pro			gga Gly		4021
Asn					Lys					Val				ctt Leu		4069
				Asp					Glu					gcc Ala		4117
aag Lys	atg Met	gat Asp	gtg Val	aat Asn	gtt Val	ggt Gly	gat Asp	att Ile	gat Asp	att Ile	gaa Glu	ggt Gly	cca Pro	gaa Glu	ggg Gly	4165

1315 1320 1325

aag ttg aag ggc ccc aag ttt aag atg cct gag atg cat ttc aag gcc Lys Leu Lys Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Ala 1330 1335 1340	4213
ccc aag atc tcc atg ccc gat gtg gac tta cac ttg aaa ggc ccc aaa Pro Lys Ile Ser Met Pro Asp Val Asp Leu His Leu Lys Gly Pro Lys 1345 1350 1355	4261
gtc aaa ggg gat atg gat gtg tct gtg ccc aag gta gaa ggt gaa atg Val Lys Gly Asp Met Asp Val Ser Val Pro Lys Val Glu Gly Glu Met 1360 1365 1370	4309
aaa gtg cca gat gtt gac att aaa ggg ccc aaa gtg gac att gat gcc Lys Val Pro Asp Val Asp Ile Lys Gly Pro Lys Val Asp Ile Asp Ala 1375 1380 1385 1390	4357
cca gat gtg gag gtt cac gac cca gat tgg cac ctg aaa atg ccc aag Pro Asp Val Glu Val His Asp Pro Asp Trp His Leu Lys Met Pro Lys 1395 1400 1405	4405
atg aaa atg ccc aag ttc agt atg cct ggc ttc aaa gca gag ggc cct Met Lys Met Pro Lys Phe Ser Met Pro Gly Phe Lys Ala Glu Gly Pro 1410 1415 1420	4453
gaa gtg gat gtg aat ctc cga aag gct gac att gat gtg tct gga ccc Glu Val Asp Val Asn Leu Arg Lys Ala Asp Ile Asp Val Ser Gly Pro 1425 1430 1435	4501
agt gtg gac act gat gct cct gat ttg gat att gag gga cca gaa gga Ser Val Asp Thr Asp Ala Pro Asp Leu Asp Ile Glu Gly Pro Glu Gly 1440 1445 1450	4549
aag ttg aaa ggc tcc aaa ttt aag atg ccc aag ttg aat ata aaa gct Lys Leu Lys Gly Ser Lys Phe Lys Met Pro Lys Leu Asn Ile Lys Ala 1455 1460 1465 1470	4597
ccc aag gtc tcc atg cca gat gtg gac ttg aat ttg aag gga ccc aaa Pro Lys Val Ser Met Pro Asp Val Asp Leu Asn Leu Lys Gly Pro Lys 1475 1480 1485	4645
ctg aag gga gag ata gat gct tct gtg cca gaa ctg gaa ggt gat ctc Leu Lys Gly Glu Ile Asp Ala Ser Val Pro Glu Leu Glu Gly Asp Leu 1490 1495 1500	4693
aga ggg ccg caa gtt gat gtc aaa ggt cct ctt gtg gaa gcg gag gtg Arg Gly Pro Gln Val Asp Val Lys Gly Pro Leu Val Glu Ala Glu Val 1505 1510 1515	4741
ccc gat gtt gat ctg gag tgt cct gat gca aag ctg aag ggc ccc aag Pro Asp Val Asp Leu Glu Cys Pro Asp Ala Lys Leu Lys Gly Pro Lys 1520 1525 1530	4789
2000	

gat gtg gac tta cac ttg aaa ggc ccc aaa gtc aaa ggg gat gtg gat 4885 Asp Val Asp Leu His Leu Lys Gly Pro Lys Val Lys Gly Asp Val Asp 1555 1560 1565 gtg tct ttg cca aaa ttg gag gga gat tta aca ggc ccc agt gtg gat 4933 Val Ser Leu Pro Lys Leu Glu Gly Asp Leu Thr Gly Pro Ser Val Asp 1575 1570 4981 gtg gag gtg cct gat gtt gag ctg gag tgt cct gat gca aag ttg aaa Val Glu Val Pro Asp Val Glu Leu Glu Cys Pro Asp Ala Lys Leu Lys 1590 1585 5029 ggg ccc aag ttt aag atg cct gag atg cac ttc aag acc ccc aag atc Gly Pro Lys Phe Lys Met Pro Glu Met His Phe Lys Thr Pro Lys Ile 1605 1600 5077 tcc atg cct gat gtg aac tta aac ttg aaa ggc ccc aaa gtc aaa ggg Ser Met Pro Asp Val Asn Leu Asn Leu Lys Gly Pro Lys Val Lys Gly 1620 1615 1625 gat atg gat gtg tct gtt ccc aaa att gga ggg aga ttt aac agg ccc 5125 Asp Met Asp Val Ser Val Pro Lys Ile Gly Gly Arg Phe Asn Arg Pro 1635 1640 cag tgt gga tgt gga ggt gcc tga tgttgagctg gctgtcgttg ttctgagggc 5179 Gln Cys Gly Cys Gly Gly Ala 1650 5239 ggcatcactc tggggtcagt ctctcccctg tcctttgagg acatacagac ctcacctatt 5299 gtttaagtgt ttgaaccagc cccgaaccca agcaacacca gagtcctcct tacatttctt cagtgagcaa accttacgca ccgtgaactt gggagtcaaa ccagctgtgc ccctcactag 5359 ccgggtaagc gcagggaggt atcgtgccac actgagcatc agttccccaa tccgaatcag 5419 gatagaacaa ttccactgtt gcttggttta cccaactgct gctgttccta atctgac 5476

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tgtgccagcc gggctctggc aggctcctgg cagc atg gca gtg aag ctt ggg 112

Met Ala Val Lys Leu Gly
1 5

		_	_	_	ctt Leu	_	_		_	_	_		-		_	160
-		-	_	_	gtg Val		_									208
					ctg Leu											256
-			•		gtg Val 60	_		-			-			_		304
_					tat Tyr											352
	-	_			aac Asn		_		-					_		400
	_			~	aac Asn		_	_		_						448
					tgg Trp											496
					cca Pro 140											544
			_		gaa Glu				-		_	_				592
					gat Asp											640
					tac Tyr											688
					ccg Pro											736
	_	_	_		atg Met 220		_			-				_	_	784

_	cgc Arg	-														832
	tgg Trp	_	_					_		_				_		880
	ctg Leu															928
_	cct Pro 280										_					976
	atg Met		_				_	-			_					1024
_	aaa Lys		_		-			_			~ ~	~	_	~		1072
	ttc Phe															1120
	ggc Gly			-			_	_						-		1168
	ctc Leu 360															1216
-	gga Gly		-	-	_			_				-	-			1264
	agg Arg															1312
	cct Pro					_										1360
	tct Ser															1408
tag *	ccaa	ata	icttt	gcc	ttgt	aaat	tt t	aaat	cctg	ıa gt	gcag	gtgaa	gaa	aatg	gtaa	1465
aaaa	aaaa	ıaa a	ıa													1477

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caccctcaag cttcaggtga gctgagcttc taacactacc atcaaagcaa ctggaacccc	180
ttgaatttga tttctggaga cgcgagcata atccttttgc aaacatctca acgctggctc	240
tccaggtgga gcacc atg gaa ggc gac tgt ctg agc tgc atg aag tat ctg  Met Glu Gly Asp Cys Leu Ser Cys Met Lys Tyr Leu  1 5 10	291
atg ttt gta ttc aat ttc ttc ata ttt ctg ggc ggg gcc tgc ctg ctg Met Phe Val Phe Asn Phe Phe Ile Phe Leu Gly Gly Ala Cys Leu Leu 15 20 25	339
gcc atc ggc atc tgg gtc atg gtg gac ccc acc ggc ttc cgg gag atc Ala Ile Gly Ile Trp Val Met Val Asp Pro Thr Gly Phe Arg Glu Ile 30 35 40	387
gtg gct gcc aat cct ctg ctc ctc acg ggc gcc tac atc ctc ctg gcc Val Ala Ala Asn Pro Leu Leu Thr Gly Ala Tyr Ile Leu Leu Ala 45 50 55 60	435
atg ggg ggc ctg ctc ttt ctg ctc ggc ttc ctg ggc tgc t	483
gtc cgt gag aac aag tgt ctg ctg cta ttt ttc ttc ctg ttc atc ctg Val Arg Glu Asn Lys Cys Leu Leu Phe Phe Phe Leu Phe Ile Leu  80 85 90	531
atc atc ttc ctg gca gag ctc tca gca gcc atc ctg gcc ttc atc ttc Ile Ile Phe Leu Ala Glu Leu Ser Ala Ala Ile Leu Ala Phe Ile Phe 95 100 105	579
agg gaa aat ctc acc cga gaa ttc ttc acc aag gag ctc acc aag cac Arg Glu Asn Leu Thr Arg Glu Phe Phe Thr Lys Glu Leu Thr Lys His 110 115 120	627
tac cag ggc aat aac gac aca gac gtc ttc tct gcc acc tgg aac tcg Tyr Gln Gly Asn Asn Asp Thr Asp Val Phe Ser Ala Thr Trp Asn Ser 125 130 135 140	675

gtc atg atc aca ttt ggt tgc tgc ggg gtc aac ggg cct gaa gac ttt Val Met Ile Thr Phe Gly Cys Cys Gly Val Asn Gly Pro Glu Asp Phe 145 150 155	723
aag ttt gca tct gtg ttt cga ctc ctg acc ctg gat agt gaa gag gtg Lys Phe Ala Ser Val Phe Arg Leu Leu Thr Leu Asp Ser Glu Glu Val 160 165 170	771
ccg gag gcc tgc tgc cgg agg gaa ccc caa agt cgg gac ggg gtc ctg Pro Glu Ala Cys Cys Arg Arg Glu Pro Gln Ser Arg Asp Gly Val Leu 175 180 185	819
ctg agc cgg gag gag tgc ctc ctg gga agg agc cta ttc cta aac aag Leu Ser Arg Glu Glu Cys Leu Leu Gly Arg Ser Leu Phe Leu Asn Lys 190 195 200	867
cag ggc tgt tac acg gtg atc ctc aac acc ttc gag acc tac gtc tac . Gln Gly Cys Tyr Thr Val Ile Leu Asn Thr Phe Glu Thr Tyr Val Tyr 205 $210 \hspace{1.5cm} 215 \hspace{1.5cm} 220$	915
ttg gcc gga gcc ctt gcc atc ggg gta ctg gcc atc gag ctt ttc gcc Leu Ala Gly Ala Leu Ala Ile Gly Val Leu Ala Ile Glu Leu Phe Ala 225 230 235	963
atg atc ttt gcc atg tgc ctc ttc cgg ggc atc cag tag agggtatggc Met Ile Phe Ala Met Cys Leu Phe Arg Gly Ile Gln * 240 245	1012
ctgaagcctg aagactcgcc ccacccacca ctgcccagca cccaatgtcc tcccgtgccc	1072
ctccccgctg tcctcttggc cccaggggag aagatgaggc catcagagat ggccaggaga	1132
agggccaggg gaatagagct attttttaa caaaacaaaa	1192
gatgtatect egeetggact eagggeaggt geegtgggtt etecagagae eecageacet	1252
ggcccaggat agcaaggctg ctctagagac aaaggaacac aaggccaggc cactatgggc	1312
agcaagaccc gggccttatt ctcatggcgt gactgtgcca gaagtgggtt cggcaggggc	1372
agcattcgag agatcaggcc ggg	1395

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<210> 82
<211> 1840
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> (264)..(1508)
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aactatttgt agagaatcac tgatccggcc tgcaagcatt ttgcacggca aaaatatcga	180
tcagtgttaa gtgaagatca cattttatat gcgatcttga cttttttgtc ttacattata	240
tttttataga ttttgttata aac atg gtg ctg gga aag gtg aag agt ttg Met Val Leu Gly Lys Val Lys Ser Leu 1 5	290
aca ata agc ttt gac tgt ctt aat gac agc aat gtc cct gtg tat tct Thr Ile Ser Phe Asp Cys Leu Asn Asp Ser Asn Val Pro Val Tyr Ser 10 15 20 25	338
agt ggg gat acc gtc tca gga agg gta aat tta gaa gtt act ggg gaa Ser Gly Asp Thr Val Ser Gly Arg Val Asn Leu Glu Val Thr Gly Glu 30 35 40	386
atc aga gta aaa tct ctt aaa att cat gca aga gga cat gcg aaa gta Ile Arg Val Lys Ser Leu Lys Ile His Ala Arg Gly His Ala Lys Val 45 50 55	434
cgc tgg act gaa tct aga aac gcc ggc tcc aat act gcc tat aca cag Arg Trp Thr Glu Ser Arg Asn Ala Gly Ser Asn Thr Ala Tyr Thr Gln 60 65 70	482
aat tac act gaa gaa gta gag tat ttc aac cat aaa gac atc tta att Asn Tyr Thr Glu Glu Val Glu Tyr Phe Asn His Lys Asp Ile Leu Ile 75 80 85	530
ggg cac gaa aga gat gat gat aat tcc gaa gaa ggc ttc cac act att Gly His Glu Arg Asp Asp Asp Asn Ser Glu Gly Phe His Thr Ile 90 95 100 105	578
cat tca gga agg cat gaa tat gca ttc agc ttc gag ctt cca cag aca His Ser Gly Arg His Glu Tyr Ala Phe Ser Phe Glu Leu Pro Gln Thr 110 115 120	626
cca ctc gct acc tca ttc gaa ggc cga cat ggc agt gtg cgc tat tgg Pro Leu Ala Thr Ser Phe Glu Gly Arg His Gly Ser Val Arg Tyr Trp 125 130 135	674
gtg aaa gcc gaa ttg cac agg cct tgg cta cta cca gta aaa tta aag Val Lys Ala Glu Leu His Arg Pro Trp Leu Leu Pro Val Lys Leu Lys 140 145 150	722
aag gaa ttt aca gtc ttt gag cat ata gat atc aac act cct tca tta Lys Glu Phe Thr Val Phe Glu His Ile Asp Ile Asn Thr Pro Ser Leu 155 160 165	770
ctg tca ccc caa gca ggc aca aaa gaa aag aca ctc tgt tgc tgg ttc Leu Ser Pro Gln Ala Gly Thr Lys Glu Lys Thr Leu Cys Cys Trp Phe 170 175 180 185	818
tgt acc tca ggc cca ata tcc tta agt gcc aaa att gaa agg aag ggc Cys Thr Ser Gly Pro Ile Ser Leu Ser Ala Lys Ile Glu Arg Lys Gly	866

190 195 200 tat acc cca ggt gaa tca att cag ata ttt gct gag att gag aac tgc 914 Tyr Thr Pro Gly Glu Ser Ile Gln Ile Phe Ala Glu Ile Glu Asn Cys 205 210 tct tcc cga atg gtg gtg cca aag gca gcc att tac caa aca cag gcc 962 Ser Ser Arg Met Val Val Pro Lys Ala Ala Ile Tyr Gln Thr Gln Ala 220 225 ttc tat gcc aaa ggg aaa atg aag gaa gta aaa cag ctt gtg gct aac 1010 Phe Tyr Ala Lys Gly Lys Met Lys Glu Val Lys Gln Leu Val Ala Asn 235 240 ttg cgt ggg gaa tcc tta tca tct gga aag aca gag acg tgg aat ggc 1058 Leu Arg Gly Glu Ser Leu Ser Ser Gly Lys Thr Glu Thr Trp Asn Gly aag ttg ctg aaa att cca cca gtt tct ccc tct atc ctc gac tgt agt 1106 Lys Leu Leu Lys Ile Pro Pro Val Ser Pro Ser Ile Leu Asp Cys Ser 270 ata atc cgc gtg gaa tat tca cta atg gta tat gtg gat att cct gga 1154 Ile Ile Arg Val Glu Tyr Ser Leu Met Val Tyr Val Asp Ile Pro Gly 285 290 gct atg gat tta ttt ctt aat ttg cca ctt gtc atc ggt acc att cct 1202 Ala Met Asp Leu Phe Leu Asn Leu Pro Leu Val Ile Gly Thr Ile Pro cta cat cca ttt ggt agc aga acc tca agt gta agc agt cag tgt agc 1250 Leu His Pro Phe Gly Ser Arg Thr Ser Ser Val Ser Ser Gln Cys Ser 320 atg aat atg aac tgg ctc agt tta tca ctt cct gaa aga cct gaa gca 1298 Met Asn Met Asn Trp Leu Ser Leu Ser Leu Pro Glu Arg Pro Glu Ala 330 335 340 cca ccc agc tat gca gaa gtg gta aca gag gaa caa agg cgg aac aat 1346 Pro Pro Ser Tyr Ala Glu Val Val Thr Glu Glu Gln Arg Arg Asn Asn 350 355 ctt gca cca gtg agt gct tgt gat gac ttt gag aga gcc ctt caa gga 1394 Leu Ala Pro Val Ser Ala Cys Asp Asp Phe Glu Arg Ala Leu Gln Gly 365 cca ctg ttt gca tat atc cag gag ttt cga ttc ttg cct cca cct ctt 1442 Pro Leu Phe Ala Tyr Ile Gln Glu Phe Arg Phe Leu Pro Pro Leu 380 tat tca gag att gat cca aat cct gat cag tca gca gat gat aga cca 1490 Tyr Ser Glu Ile Asp Pro Asn Pro Asp Gln Ser Ala Asp Asp Arg Pro 395 400 tcc tgc ccc tct cgt tga aggaac acttggttga atcaagttga tgtgggttcc 1544 Ser Cys Pro Ser Arg 410 415

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<211> 800

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (509)..(685)

<400> 83

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50

676

732

caa gaa cag ttt ctt ctg gat tcc tta ttt gat tta ttt aac cta att

Gln Glu Gln Phe Leu Leu Asp Ser Leu Phe Asp Leu Phe Asn Leu Ile

ata ttc taa tattgca aatattacca taagtgggta aaagtaaaat tcctcttctg

## Ile Phe \*

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tgc ccc atg tgt agg gaa ttt ttc tct gag aga gca gat ctt ttt atg

Cys Pro Met Cys Arg Glu Phe Phe Ser Glu Arg Ala Asp Leu Phe Met

5 10 15 20

1

cat cag aaa att cac aca gct gag aag ccc cat aaa tgt gac aag tgt 692 His Gln Lys Ile His Thr Ala Glu Lys Pro His Lys Cys Asp Lys Cys 25 30 35

gat aag ggt ttc ttt cat ata tca gaa ctt cat att cat tgg aga gac 740 Asp Lys Gly Phe Phe His Ile Ser Glu Leu His Ile His Trp Arg Asp 40 45 50

cat aca gga gag aag gtc tat aaa tgt gat gat tgt ggt aag gat ttt 788
His Thr Gly Glu Lys Val Tyr Lys Cys Asp Asp Cys Gly Lys Asp Phe
55 60 65

	act Thr 70															836
	ccc Pro															884
	ctt Leu															932
	agt Ser															980
cat His	cag Gln	aga Arg 135	gtc Val	cac His	acc Thr	gga Gly	gag Glu 140	aag Lys	ccc Pro	ttt Phe	aaa Lys	tgt Cys 145	gaa Glu	gag Glu	tgt Cys	1028
	aag Lys 150															1076
cac His 165	aca Thr	gga Gly	gag Glu	aaa Lys	ccc Pro 170	tat Tyr	aaa Lys	tgt Cys	tat Tyr	gag Glu 175	tgt Cys	Gly ggg	aag Lys	gcg Ala	ttc Phe 180	1124
	cag Gln															1172
	ccc Pro															1220
	ctg Leu															1268
	gat Asp 230															1316
	cag Gln															1364
ata Ile	taa *	aacg	gttti	iga t	caaga	agttt	a aa	aatct	taaa	a aco	ccata	aagt	gcca	actag	gga	1420
agga	aaaco	cct g	gtata	ataco	ct a	catto	gacco	c aag	gaaat	att	tace	gcaat	cc o	ctago	cagaac	1480
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aggttgactt tgaatgtgga cctctgagca tccacgcagg atggctctca ggtcccagtc 1600 1660 acagacgtcg cttcctggga ttccagcacg atgcctccat agttgaaaga ctacacaaaa agccacaatc attgcccggc ctcctgagtc accttctatc tatactttgc ttaaaagcta 1720 1780 tcccagatac tcccccttga ggagetcatg cccttccttc ctctttattc gageatactg gcaatgcatt ggaaaacaga cagctcccac taagatcacg ttctggtatt tctgaggtta 1840 1900 acacttgatt tagcccctac atatctttcc atatatccta ttatttctga atatatgtcc tcaaaatccc cataaatatc catcccttcc tagatggcat taactttcat tttagatttt 1960 2020 aggtgactca taattcccat tcacttagcc tatcagaaaa gtcattggca gacatatatg tccttgaacc ttttttattt gtgtggattc tgctcatcac tgtctctgtt agacttattt 2080 2140 tgtagtggct gcatcacata tttttcactt gaattttttt ggaaatagct gaatgtaaat agcagggagg aagaagcaag caaagtgaga gcttttcttc atccagaatt gccctctggg 2200 2260 ctcctttggt aacagatgga gctccttcct agctagggag accttatgag aagtggatgg 2320 taggaggagt cactaatgtt tcaatctcta tttctgtaat cttgggcaat aatgcatagg 2380 agttcttgat accccttcat tgattactgt gtatcagttc tttgttaggc atgaacgtct 2440 ttattaatcc atcattcttt tcttcattca acaaatatgt attgaacacc tcctatatgc 2500 caqqcactqt gctaggtgct gggaatacca ctgatgagac agacaaggtc cctactcttg tggagtttac ttctggtgga ggagacagat gataagtaaa caaataaata atgtagtttg 2560 2620 agatagtgat taagtgctat gaagaaaata aactagggtg atgattttag tggtggggtg gggtggggt ggggttacat tagctagtgg tcagggaggc ctttccgcgg tgggatgttg 2680 2740 agctgaggcc ggaggagaag tagcagtcgc tggcagagca cacaggctgc tctgggggat 2800 gagctggtgc gtttaaggaa caggccagca ctggcattcg caagcagtgg ggaaggggag 2860 agatgccgag gtggtcagta tcctgacttt cagaggcctt tttttgtttg ttttaatttt 2885 tgctagattg atattaaaaa aaaaa

<sup>&</sup>lt;210> 85

<sup>&</sup>lt;211> 1685

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (66)..(1382)

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_				-	_	aag Lys	-	_		_		_			-	155
						acc Thr				-					-	203
						gaa Glu										251
						att Ile										299
	_	_	_	_		caa Gln 85										347
						aca Thr										395
		_			-	gaa Glu						-		_	_	443
_			-	_	_	att Ile		~	~	~ ~		_		_	•	491
_	_	_		-	_	caa Gln	_	_		_	_		_			539
						ttt Phe 165										587
						atg Met										635
						aac Asn										683
aaa	aag	ctt	gac	aat	ttg	cag	tgc	ttg	tac	tgt	gag	aag	acc	ttc	agg	731

Lys	Lys	Leu	Asp 210	Asn	Leu	Gln	Cys	Leu 215	Tyr	Cys	Glu	Lys	Thr 220	Phe	Arg	
_						gat Asp		_				-		_	_	779
						gaa Glu 245										827
						tgg Trp										875
						gaa Glu										923
	_		_	_	_	tta Leu		_	_							971
	_	_		_		atg Met										1019
						gga Gly 325										1067
						caa Gln										1115
		_				aaa Lys	_	-		_			_	-	_	1163
						ctc Leu										1211
						tat Tyr										1259
						ctg Leu 405										1307
				-		aca Thr										1355
						cta Leu		taa *	gagt	a ct	tgaa	aaco	tag	gaaga	aac	1407

<210> 86

tac	cacagaa	gcaatttttc	atgtttttct	cctatgagac	agatatgaaa	gaacaattta	1467
aat	ttgaaca	tcaacaaaag	attggtcctt	ggtgaaataa	acttttcaaa	aatgaatgtt	1527
ctt	ttcaaaa	aataaagtag	aaaaatgcac	ttactaagaa	catgaaaaaa	aatgaagtag	1587
gaa	aataaga	tgaagacttt	gtattttggc	tgtaaagttt	tattgtgtga	tcatcttaaa	1647
tta	tctcact	tcattaaact	cataattata	tatagaaa			1685

<211> 1094 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (59)..(595) <400> 86 atttcgtggc ttgccgggcg gccccaggcg gctgggcacg caccccaaga aggagccc 106 atg gag gcg ctg aac acg gcg cag ggc gcg cgc gac ttc atc tac agc Met Glu Ala Leu Asn Thr Ala Gln Gly Ala Arg Asp Phe Ile Tyr Ser 154 ctq cac tcc acq qaq aqq agc tgc ctg ctc aaa gag ctg cac cgc ttc Leu His Ser Thr Glu Arg Ser Cys Leu Leu Lys Glu Leu His Arg Phe 202 gag tot att god att god daa gaa aaa ttg gaa got coa cod coc acc Glu Ser Ile Ala Ile Ala Gln Glu Lys Leu Glu Ala Pro Pro Pro Thr 40 cca gga cag ctg aga tat gta ttc atc cac aat gcg ata cct ttc ata 250 Pro Gly Gln Leu Arg Tyr Val Phe Ile His Asn Ala Ile Pro Phe Ile 50 55 298 ggg ttt ggc ttt ttg gat aat gca att atg att gct gga acc cat Gly Phe Gly Phe Leu Asp Asn Ala Ile Met Ile Val Ala Gly Thr His 65 att gaa atg tct att gga att att ttg gga att tca act atg gca gct 346 Ile Glu Met Ser Ile Gly Ile Ile Leu Gly Ile Ser Thr Met Ala Ala 85 95 gct gct ttg gga aat ctt gtg tca gat cta gct gga ctt gga ctt gca 394 Ala Ala Leu Gly Asn Leu Val Ser Asp Leu Ala Gly Leu Gly Leu Ala 100 105 110 442 ggc tac gtt gaa gca ttg gct tcc agg tta ggc ctg tca att cct gat Gly Tyr Val Glu Ala Leu Ala Ser Arg Leu Gly Leu Ser Ile Pro Asp 120 125 115

ctc aca cca aag caa gtt gac atg tgg caa aca cgt ctt agt aca cat Leu Thr Pro Lys Gln Val Asp Met Trp Gln Thr Arg Leu Ser Thr His 130 135 140	490
ttg ggc aaa gct gtt ggg gtg act att ggc tgc att cta gga atg ttt Leu Gly Lys Ala Val Gly Val Thr Ile Gly Cys Ile Leu Gly Met Phe 145 150 155 160	538
cct tta att ttc ttt gga gga ggt gaa gaa gat gaa aaa ctg gaa acg Pro Leu Ile Phe Phe Gly Gly Glu Glu Asp Glu Lys Leu Glu Thr 165 170 175	586
aaa agt taa teetett agaataeeta taaaaagatg taaaetaatg taeeteagta Lys Ser *	642
attaaatatg ctgtcacaac atttaggaat taagacagta acagtataga tatgggatca	702
aataatttag catgtattat ggaaaacact aacttattgt ggcttgatct tcttaggaca	762
tcttttttaa aaagctgttt agtatcattt tgtgtatatt gttgaaatgc tttttcatca	822
atagcagtca acattttatc ctttctttt atattcataa tgttatttaa gtgtcattga	882
tgtactgtat tgacttgggg tttgcttatt tgttacttaa catgtgtaca tgcatgaaag	942
catttttcgt tgttccctga tagttacatt tcaaccttgg gatttttcca aattacttaa	1002
gatgtttaat gtcagttaaa gatttttta ccctcttttt gggaacatca attttgtact	1062
gttatgcagt aaacatttat aataatataa aa	1094

<210> 87

<211> 1046

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (272)..(1024)

<400> 87

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gaaacccacg aggggacgcg gccgaggagg gtcgctgtcc acccgggggc gtgggagtga 120
ggtaccagat tcagcccatt tggccccgac gcctctgttc tcggaatccg ggtgctgcgg 180
attgaggtcc cggttcctaa cggtgggatc ggtgtcctcg ggatgagatt tggcgtttcc 240
tcggggcttt ggtgggatcg gtgtcctcag g atg aga ttt agg gtt tcc tcg
Met Arg Phe Arg Val Ser Ser
1 5

					ggc Gly											340
	-		-		gat Asp				_	-						388
					tgc Cys 45											436
					ggg Gly											484
					ggt Gly											532
_				_	ctt Leu		_	_			_				-	580
		-	-		ctc Leu									_		628
					ctc Leu 125											676
_					gag Glu	_	_	_			_	_		_	-	724
		_			gtc Val		_	_		_	_		-			772
					ctg Leu											820
					agc Ser								_	-		868
					aag Lys 205											916
			_		tct Ser		-		-		_	_	_	_		964

ggg ctc tgt ctc gct ggc ttg ccc tgg gaa tta gga gct cta gct ggg Gly Leu Cys Leu Ala Gly Leu Pro Trp Glu Leu Gly Ala Leu Ala Gly 235 240 245	1012
cct ggt gta taa tgctctccga aaaaaaaaaa aa Pro Gly Val * 250	1046
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<221> CDS <222> (19)(1830)	
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tct gct ata ttc cat aca att aga ttt gtt ctt gcc tca aga ctt cag Ser Ala Ile Phe His Thr Ile Arg Phe Val Leu Ala Ser Arg Leu Gln 15 20 25	99
tct gat tgg atg ttg atg ctg tat ttt gca cat act cat ttg act gtg Ser Asp Trp Met Leu Met Leu Tyr Phe Ala His Thr His Leu Thr Val 30 35 40	147
aca gtc acc att ggg ttg ctt ttg att cca aag ttt tca cat tca agc Thr Val Thr Ile Gly Leu Leu Ile Pro Lys Phe Ser His Ser Ser 45 50 55	195
aat aac cca cga gat gat att gct aca gaa gca tat gag gat gag cta Asn Asn Pro Arg Asp Asp Ile Ala Thr Glu Ala Tyr Glu Asp Glu Leu 60 65 70 75	243
gac atg ggc cga tct gga tcc tac ctg aac agc agt atc aat tca gcc Asp Met Gly Arg Ser Gly Ser Tyr Leu Asn Ser Ser Ile Asn Ser Ala 80 85 90	291
tgg agt gag cac agc ttg gat cca gag gac att cgg gac gag ctg aaa Trp Ser Glu His Ser Leu Asp Pro Glu Asp Ile Arg Asp Glu Leu Lys 95 100 105	339
aaa ctc tat gcc caa ctg gaa ata tat aaa aga aag aag atg atc aca Lys Leu Tyr Ala Gln Leu Glu Ile Tyr Lys Arg Lys Lys Met Ile Thr 110 115 120	387
aac aac ccc cac ctc cag aaa aag cgg tgc tcg aag aag ggc cta ggt Asn Asn Pro His Leu Gln Lys Lys Arg Cys Ser Lys Lys Gly Leu Gly 125 130 135	435

		atc Ile											483
_	_	tct Ser											531
		gcc Ala			_								579
		tcc Ser 190											627
		cac His											675
_	-	cta Leu		-	_								723
	_	gaa Glu	-	_									771
		gag Glu											819
-	_	gct Ala 270			_		_					_	867
	_	atg Met	_	_		~	-	-	-	_	_		915
		ctt Leu											963
		aaa Lys											1011
		tca Ser		_				-		_			1059
		aat Asn 350											1107

					gtc Val											115
					atg Met 385											120
					gac Asp											125
					gta Val											129
					aag Lys											134
-					tcc Ser								_	_	_	139
					caa Gln 465											144
_			_		cca Pro	-			_		_		-			149
					gca Ala											153
_					gta Val											158
					gaa Glu											163
					tca Ser 545											168
					cct Pro											173
		_	_		gct Ala											177
aag	ata	gca	ggg	cct	agg	aaa	gaa	gag	gtc	tgg	gat	agt	ttt	aaa	gtg	182

Lys Ile Ala Gly Pro Arg Lys Glu Glu Val Trp Asp Ser Phe Lys Val 590 595 600

tag catc tccaggaaga agaggaaaag gagggaaccc cggattggat atgagacaga	1884
agatataaga atcaaatatt cccaaggagg atttgtcaat caaggaaaac atgacagatg	1944
gtgaggtaaa gtcaaaggca tgggtagaag aggaccaggg gggcaagagc aacaacgtca	2004
taatggagaa gtcagacttt ggtcaagaaa gtccttccct tggtaacact aggaaaatct	2064
ttccatttca gcatgtttaa ggaaaatagc ccacaatgtc tgccctgatc aatatgtatc	2124
catgggactt tgaagatcct aagccaggta aaccaggaga cacagaagac gtaccagatt	2184
tgcaaagaaa gaaaaggtat aagacatata taactgaaat tctaagtagc tgaccgagaa	2244
gaacttactt tacctattta accttgatag cactgctaac ttaatgcatc ccaaaaatat	2304
cttttatatt aatgattgct ctcattttct tataaatgta tgtttcagta tatcgttgtg	2364
tctcatattc aagcattcca gattgtataa tttttgcaaa taactttggt attatgtgac	2424
acaacacatt tatgcaatct gcagctattc aattgttatt gcaccttaca gaatacctgc	2484
tatctatcaa ctttagttga ttcttgaagt acagtaagct ttctctggct tgggaagcca	2544
taactgttac tataaaaact tttagttttg gctgtggttt atatattgtg actttgaatt	2604
tgactctatt atttcacatc atggtttgtt atactgtctt aatcagggtt ttttatacaa	2664
gttgagttac ttgttttgca cttcttgtta ggactcagaa gctttattaa tattggagat	2724
caagtggtcc tacttagtca tatgtctcaa taagttaagg acaacttatc cgttgtttat	2784
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tatttcctac ttagcagcat ttccaaagga agaagctaag agtgagaaaa atataccgtg	2904
cattattatt actattggaa agggaagact ctagggatga cataagaatt atagcagtac	2964
tataaaccca ggaagtttgc ctttcaaaaa aaaacacagg tagctcctga tagcactttc	3024
aagggattat ttttttaaag agaaaaatta tggtagcatc aagatcattg tatggatata	3084
tttttattat gtgtactgaa aatacagtat tttaaaaatac cttaaagtat ttattctcat	3144
aaactcttat tcattgcttc agctacaggt agaacttgct gggctcaaat cccaaagagg	3204
ttttataacc ttatttattc aaaacctata aggtggtatg gaatcttcat tctcccaagc	3264
actggaaaat gtctaagtcc tgcaaattgc cattgtgagc cacttgctcg acatgtaaca	3324
tgtaaggtcc atttgcaaag caaagcagcc cccaaagcat attttataaa gcttattgca	3384

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<sup>&</sup>lt;210> 89

<sup>&</sup>lt;211> 2778

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<221> CDS <222> (250)..(2664)

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Asp	Val 175	Lys	Gln	Val	Lys	Glu 180	Leu	Ile	Ser	Leu	Gly 185	Ala	Asn	Val	Asn	
					ggt Gly 195											864
			_	_	gct Ala	_				-	-		_	_		912
					gat Asp	_	_									960
_			-	_	ata Ile	_	_	_			_		-			1008
			_		aaa Lys				-			-	-			1056
					ttg Leu 275											1104
_	_	~	_		aca Thr	_		_		-			_			1152
					aat Asn											1200
	_	_	_		cag Gln				_							1248
					gag Glu											1296
					agg Arg 355											1344
					gaa Glu											1392
					tca Ser											1440
					act Thr											1488

405 400 410 1536 aaa aag att tot act toa tgt too gto atc oot gaa aca toa aat tot Lys Lys Ile Ser Thr Ser Cys Ser Val Ile Pro Glu Thr Ser Asn Ser 420 1584 gat atg caa acc aaa aag gaa tat gta gtt tca ggt gaa cac aaa cag Asp Met Gln Thr Lys Lys Glu Tyr Val Val Ser Gly Glu His Lys Gln 440 aaa ggc aaa gtt aaa aga aaa ttg aaa aat cag aat aaa aat aaa gag 1632 Lys Gly Lys Val Lys Arg Lys Leu Lys Asn Gln Asn Lys Asn Lys Glu 455 1680 aac caa gag cta aag caa gaa aag gaa gga aaa gaa aat aca aga ata Asn Gln Glu Leu Lys Gln Glu Lys Glu Gly Lys Glu Asn Thr Arg Ile 470 1728 aca aac ttg aca gta aat act gga cta gat tgt tca gaa aag acc aga Thr Asn Leu Thr Val Asn Thr Gly Leu Asp Cys Ser Glu Lys Thr Arg 480 485 gag gag gag aac ttt agg aaa tct ttt agc cca aaa gat gat act tca 1776 Glu Glu Gly Asn Phe Arg Lys Ser Phe Ser Pro Lys Asp Asp Thr Ser 1824 tta cat tta ttt cat att tcc act ggt aaa tct ccc aaa cat tct tgt Leu His Leu Phe His Ile Ser Thr Gly Lys Ser Pro Lys His Ser Cys 1872 gga tta agt gaa aaa cag tca aca cca cta aaa caa gaa cat act aaa Gly Leu Ser Glu Lys Gln Ser Thr Pro Leu Lys Gln Glu His Thr Lys 1920 aca tgt tta tca cca gga agt tct gaa atg tca tta cag cct gat ctt Thr Cys Leu Ser Pro Gly Ser Ser Glu Met Ser Leu Gln Pro Asp Leu 550 545 gtt cgg tat gat aat aca gaa tct gaa ttc ttg cca gaa agt tca agt 1968 Val Arg Tyr Asp Asn Thr Glu Ser Glu Phe Leu Pro Glu Ser Ser Ser 560 565 2016 gta aaa tct tgt aag cat aag gaa aaa agc aaa cat cag aaa gat ttc Val Lys Ser Cys Lys His Lys Glu Lys Ser Lys His Gln Lys Asp Phe 575 580 cac tta gaa ttt ggt gaa aaa tca aat gcc aaa ata aag gat gaa gat 2064 His Leu Glu Phe Gly Glu Lys Ser Asn Ala Lys Ile Lys Asp Glu Asp 590 595 600 605 cat agt cca aca ttt gaa aat tca gat tgc aca ctg aaa aaa atg gat 2112 His Ser Pro Thr Phe Glu Asn Ser Asp Cys Thr Leu Lys Lys Met Asp 610 615 aaa gaa ggt aaa aca tta aaa aaa cat aaa ttg aag cat aaa gag agg 2160 Lys Glu Gly Lys Thr Leu Lys Lys His Lys Leu Lys His Lys Glu Arg 625 630

gaa aaa gaa aag cat aaa aaa gaa att gaa ggt gaa aag gaa aaa tac Glu Lys Glu Lys His Lys Lys Glu Ile Glu Gly Glu Lys Glu Lys Tyr 640 645 650	2208
aaa act aag gat agt gcc aaa gaa ctg cag agg agt gtg gaa ttt gat Lys Thr Lys Asp Ser Ala Lys Glu Leu Gln Arg Ser Val Glu Phe Asp 655 660 665	2256
aga gaa ttt tgg aaa gag aat ttt ttt aaa agt gat ga	2304
ctc ttt tta aat atg gaa cat gaa tcc tta aca tta gaa aaa aaa tca Leu Phe Leu Asn Met Glu His Glu Ser Leu Thr Leu Glu Lys Lys Ser 690 695 700	2352
aaa ttg gaa aaa aac atc aaa gat gat aaa tca acc aag gaa aag cat Lys Leu Glu Lys Asn Ile Lys Asp Asp Lys Ser Thr Lys Glu Lys His 705 710 715	2400
gtg tca aaa gag agg aac ttt aaa gag gaa cga gac aag att aaa aag Val Ser Lys Glu Arg Asn Phe Lys Glu Glu Arg Asp Lys Ile Lys Lys 720 725 730	2448
gaa agc gag aaa tct ttt agg gag gaa aaa ata aaa gat cta aaa gaa Glu Ser Glu Lys Ser Phe Arg Glu Glu Lys Ile Lys Asp Leu Lys Glu 735 740 745	2496
gag aga gaa aac ata ccc aca gat aaa gac tca gaa ttt act tct ttg Glu Arg Glu Asn Ile Pro Thr Asp Lys Asp Ser Glu Phe Thr Ser Leu 750 765	2544
ggt atg agt gcc att gag gaa tct ata ggg ctt cat tta gtg gaa aag Gly Met Ser Ala Ile Glu Glu Ser Ile Gly Leu His Leu Val Glu Lys 770 775 780	2592
gaa ata gac att gaa aaa caa gaa aag cat ata aag gaa aat aaa aaa Glu Ile Asp Ile Glu Lys Gln Glu Lys His Ile Lys Glu Asn Lys Lys 785 790 795	2640
aaa aaa agg cgg ccg ctc tag agtatccctc gaggggccca agcttacgcg Lys Lys Lys Gly Arg Pro Leu * 800 805	2694
tacccagctt tcttgtacaa agtggtccct atagtgagtc gtattataag ctggcgcctg	2754
cgcagctagt caacctctca cctt	2778

<sup>&</sup>lt;210> 90

<sup>&</sup>lt;211> 1070

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

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ccaattatgt ttaaatactt caaacagcaa atactacagt ttatctcaat gaatataata	120
accattcctg ctgggcgcag tggctcatgc ctttaatccc agtcattaag gaggctgagg	180
tgggaagatt gcttgaaacc aggagattgc ctcaggcctg ggcaacatgg tgagacctct	240
tatctcaaaa aatcaaaata aaaaattagc tgggcatggt ggctcatccc tgtagcccca	300
gcttctcaag aggctgaggt gggaggatag cttcagccta ggagacagaa gctgcagtga	360
gctatgatca caccactaca ctccagcctg gacaacagaa agagaccttg tctctaaaaa	420
caaaacaaaa caatcaaaca aaaaagtact cctgaattta agtattgatg gctatgggaa	480
ttgcttccta acctgtttga aaaatgtgtt aactgttaca tattttgaga actgcagcac	540
tcagtgaagc tttgttaaag ggaatgagga gtttaggccc cagcaggcaa accacttcac	600
agtgctagga tgaagagctc acactcaggg acttcgagag tgaatcaact actttcgtta	660
actcaatgtt aaatgagaat aacatcaacc ttggatggtt gtggtgagaa tcaaatgaaa	720
tgacat atg gga aaa cct ttg tca cat gtt aca caa ttg acg gca act Met Gly Lys Pro Leu Ser His Val Thr Gln Leu Thr Ala Thr 1 5 10	768
aca gct tta ggt aga att tca act tct aat ttt tac tac tat gca aat Thr Ala Leu Gly Arg Ile Ser Thr Ser Asn Phe Tyr Tyr Tyr Ala Asn 15 20 25 30	816
tat cag aat att tat gat gtt aac ttt tta aaa agg ttt tta aat aga Tyr Gln Asn Ile Tyr Asp Val Asn Phe Leu Lys Arg Phe Leu Asn Arg 35 40 45	864
aac ttt att taa ata aatgaactct tctcaacccc aaaacccagc ttctgatctt Asn Phe Ile * 50	919
gactaagttc ataattactc agggaaaaac actgctggtt ccttataagc cactgtgctg	979
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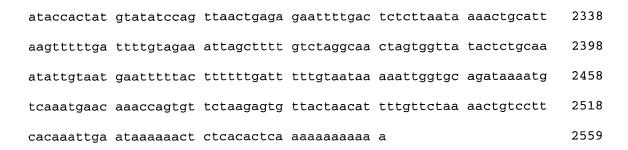
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40

35

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582

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Leu Asp Lys Leu Trp Thr Leu Val Ser Glu Gln Thr Arg Val Asn Ala 85 90 95													
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			_	-		cat His	~ ~			-	_				-	414
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						ata Ile 220										846
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gat gaa gta cga tt Asp Glu Val Arg Le 630				
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20 25 30 35

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ctt ttt t Leu Phe S 100	-		ı Ile	-		-		-		-			391
gca aac a Ala Asn A	-	_	_		_				-				439
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ata aaa t Ile Lys L 1	_	_			-					_	_		535
gcc act t Ala Thr S 165			-	~	-	_	-		-	-	-		583
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-		_			ccc Pro	_										691	
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								ccc Pro 495								1	603
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] go .] Al	a aaa .a Lys															163
	t cat p His															211
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_ Le	g ctt u Leu 5															307
	g aag u Lys															355
	a tca s Ser															403
	a aga u Arg															451
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gt Va 13	t ctg l Leu 5	gat Asp	ctc Leu	tgt Cys	gct Ala 140	gct Ala	cct Pro	gga Gly	ggg Gly	aaa Lys 145	tta Leu	ata Ile	gct Ala	ctg Leu	ctg Leu 150	547

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1 5 10

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60

852

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Leu Lys Glu Ile Gly Phe Ile Asn Tyr Tyr Gly Met Gln Arg Phe Gly

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			-	-	atg Met	-			_			_			-	948
-	-			_	gtt Val		-	~	~	-	~ ~	~	_			996
-			-	-	ctc Leu 115	_				-			_		_	1044
		_		_	gga Gly						-	_			-	1092
	-				ata Ile		-			_		_				1140
					gtg Val				_	_	_	-			-	1188
					cct Pro											1236
					gag Glu 195	-	_	-	-							1284
					ttg Leu											1332
					tac Tyr											1380
			_	_	cac His			_	-			_			_	1428
					att Ile	-		_		_	_		-	_	_	1476
					aaa Lys 275											1524

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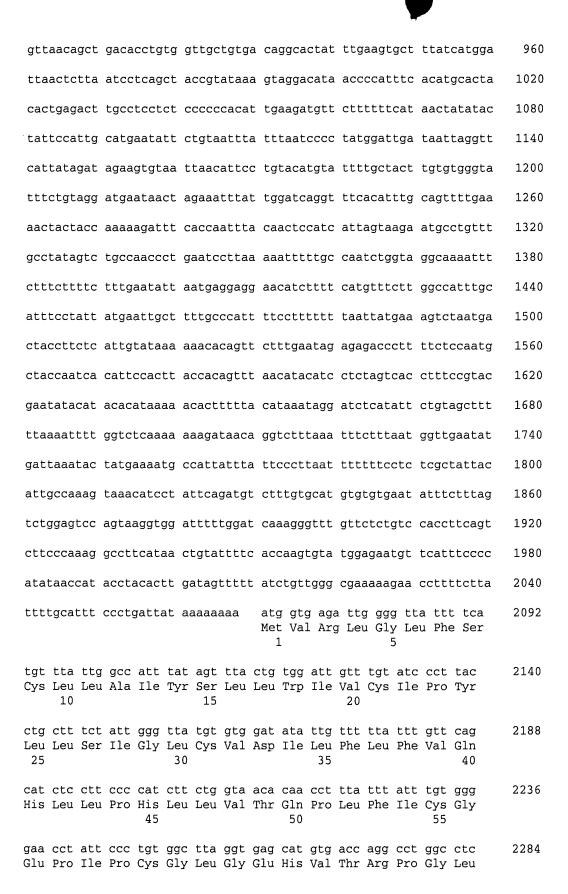
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												agc Ser 55			195
å												gac Asp			243
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												gtg Val			387
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												gaa Glu			483
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soft from And 3: 31 HV None Sout South	aaaa																2761
and thus may a		<21 <21	.0> : .1> { .2> I .3> I	321 ONA	sapi	.ens											
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	gaa Glu	gtc Val	atg Met	aaa Lys	att Ile	aaa Lys	gca Ala	gaa Glu	ata Ile	aag Lys	gct Ala	gcc Ala	aaa Lys	gca Ala	gat Asp	gaa Glu	295





75 80 85

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cat ccc tca gat gaa aaa tat tca ggt tta aca gca agc tca aaa aag His Pro Ser Asp Glu Lys Tyr Ser Gly Leu Thr Ala Ser Ser Lys Lys 105 110 115	391
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tca caa aaa caa att aaa aat agt agc ctc ctt tct ttt gac aac gaa Ser Gln Lys Gln Ile Lys Asn Ser Ser Leu Leu Ser Phe Asp Asn Glu 135 140 145 150	487
gat gaa aat gag taa gtgtaaatat tttgaattta gtctactttg aaagtatatg Asp Glu Asn Glu * 155	542
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tgt Cys 40	ggc Gly	tgg Trp	aag Lys	gat Asp	cag Gln 45	ttg Leu	aag Lys	gca Ala	cac His	tgt Cys 50	aaa Lys	gag Glu	gta Val	att Ile	aaa Lys 55	316
gaa Glu	aaa Lys	gga Gly	cta Leu	gaa Glu 60	cac His	gtt Val	act Thr	gtt Val	gat Asp 65	gac Asp	ttg Leu	gtg Val	gct Ala	gaa Glu 70	atc Ile	364
act o																412
cta ( Leu (														taa *	gat	460
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gctgg atg g Met A 1	cg (	gct g	gct g	gat (	gca d	ege t	tgg a	aac d	cat o	gtg	tgg (	gtc g	ggc a	acc o	gag	476 524
act g	gg a	atc t	tg a	aaa q	ggg g	gta a	aat d	ctt d	cag d	cga	aaa (	cag q	gcg g	gcg a	aac	572

Thr	Gl3	/ Ile	e Let 20	ı Lys	≅ Gl∑	/ Val	l Ası	ı Lei 25		n Ar	g Ly:	s Glr	n Ala		a Asn	
ttc Phe	aco Thr	g gcc Ala 35	ı Gly	gga Gly	a cag / Glr	g cco	g cgg Arg 40	g Arg	g gag g Glu	g gag ı Glu	g gca ı Ala	a gtg a Val 45	. Ser	gco Ala	c ctg a Leu	620
tgt Cys	tgg Trp 50	Gly	acc Thr	. Gl <sup>y</sup>	ggc Gly	gag Glu 55	ı Thr	cag Glr	g ato Met	g cto Leu	g gtg 1 Val 60	l Gly	tgc Cys	gcg Ala	g gac Asp	668
agg Arg 65	acg Thr	gtg Val	aag Lys	cac	ttc Phe 70	Ser	acc Thr	gag Glu	gat Asp	ggc Gly 75	ı Ile	a ttc Phe	cag Gln	ggt Gly	cag Gln 80	716
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gtt Val	tat Tyr 210	gat Asp	cca Pro	gca Ala	tcc Ser	ccc Pro 215	cag Gln	cgc Arg	cgg Arg	cca Pro	gtc Val 220	cta Leu	gag Glu	acc Thr	acc Thr	1148
tat ( Tyr ( 225	gga Gly	gag Glu	tac Tyr	cca Pro	cta Leu 230	aca Thr	gcc Ala	atg Met	Thr	ctc Leu 235	act Thr	ccg Pro	gga Gly	ggc Gly	aac Asn 240	1196
tca ( Ser V	gtg /al	att ( Ile '	gtg Val	gga Gly	aac Asn	act Thr	cat His	ggg Gly	cag Gln	ctg Leu	gca Ala	gaa Glu	att Ile	gac Asp	ctt Leu	1244

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cgg Arg	caa Gln	Gly aaa	cgt Arg 260	cta Leu	ctg Leu	ggc	tgt Cys	ctg Leu 265	aag Lys	Gly	ctg Leu	gca Ala	ggc Gly 270	agt Ser	gtg Val		1292
cgt Arg	ggg Gly	ttg Leu 275	cag Gln	tgc Cys	cac His	cct Pro	tca Ser 280	aag Lys	cct Pro	cta Leu	cta Leu	gcc Ala 285	tcc Ser	tgt Cys	ggc Gly		1340
ttg Leu	gac Asp 290	aga Arg	gtc Val	ttg Leu	agg Arg	ata Ile 295	cac His	agg Arg	atc Ile	cag Gln	aat Asn 300	cca Pro	cgg Arg	ggt Gly	ctg Leu		1388
gag Glu 305	cat His	aag Lys	gtt Val	tat Tyr	ctc Leu 310	aag Lys	tct Ser	caa Gln	ttg Leu	aac Asn 315	tgc Cys	ctc Leu	ctc Leu	ttg Leu	tca Ser 320		1436
ggc Gly	agg Arg	gac Asp	aac Asn	tgg Trp 325	gag Glu	gat Asp	gag Glu	ccc Pro	caa Gln 330	gag Glu	cct Pro	caa Gln	gaa Glu	ccc Pro 335	aac Asn		1484
aag Lys	gtg Val	ccc Pro	cta Leu 340	gaa Glu	gac Asp	aca Thr	gag Glu	aca Thr 345	gat Asp	gaa Glu	ctt Leu	tgg Trp	gca Ala 350	tcc Ser	ttg Leu	:	1532
gag Glu	gca Ala	gct Ala 355	gcc Ala	aag Lys	cgg Arg	aag Lys	ctc Leu 360	tcg Ser	ggt Gly	ttg Leu	gag Glu	cag Gln 365	ccc Pro	caa Gln	gga Gly	-	1580
gct Ala	ctc Leu 370	caa Gln	acg Thr	aga Arg	cgg Arg	aga Arg 375	aag Lys	aag Lys	aag Lys	cgg Arg	cct Pro 380	ggg Gly	tcc Ser	acc Thr	agc Ser	2	1628
ccc Pro 385	tga *	cgcc	cctg	tg c	ccac	tttg:	t aa	ataa	actg.	r ctg	jaaca	.ccc	aaaa	aaaa	.aa	1	L684
aaa																1	.687
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						atg Met										261
						cgt Arg										309
						aac Asn										357
						gtg Val 90										405
						ttt Phe										453
						cct Pro										501
						tta Leu										549
						acc Thr										597
						cac His 170										645
gag Glu 180	gtt Val	gtc Val	aaa Lys	cag Gln	aat Asn 185	gtt Val	gct Ala	gcc Ala	ttt Phe	gag Glu 190	cgt Arg	cgg Arg	gca Ala	gcc Ala	acc Thr 195	693
						gcc Ala										741
		cag Gln		tga *	ggca	aaggg	gat t	geto	ccctg	ga co	ctcc	ettet	aco	cca	cttc	796

cctacacaat tctcttattt atttggtttg gctcctgttc caatttgaaa ggagtctgtg 856 ttcataatac tgtttctcct ctcaatttcc cagaaattgg gttctatgct ggctggaaat 916 gttgggggaa agagaaggca aaggatgtgg aaatgagatg tgcttaggaa agggtcaggc 976 ccatcgtagg agcaccatat gcctgcagcc ttttcactac gaattagaat aaggactatg 1036 1096 tggttgtctc tggaccttat caagacacct tagtgtctga ccaggggacg atagtaactt 1156 ttctaaggat tgaataaatt gagcttttct tctggcacag aggtactgag tggtaagtaa cttttaccct gcctgagatt cctcaggaga aaaggcaacc tgcctccagc ctgaaataca 1216 1276 taaagcctca ttttaagact gtaagtccat gctgcctggc tactagagag caaggggctt tcttaccacc agtgctgagg agaaaagtac tgaacggaaa cggagttgtc tttgtactct 1336 tgagttgtac cttattcttc cacttggcct gagtttttat aaaatttcaa taaattgtga 1396 1416 cagtgtgaaa aaaaaaaaa

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cca gcc atg gtc aac ccc acc atg ttt ttc cac att gct gtc gat ggc

Pro Ala Met Val Asn Pro Thr Met Phe Phe His Ile Ala Val Asp Gly 25 30 35	
gag ccc ttg ggc tgt gtc tcc ttc gag ctg ttt gca gac aag gtt cca Glu Pro Leu Gly Cys Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro 40 45 50 55	556
aag aca gca gaa aat ttc cat gct ctg agc act gga gaa aaa gga ttt Lys Thr Ala Glu Asn Phe His Ala Leu Ser Thr Gly Glu Lys Gly Phe 60 65 70	604
ggt tat aag ggt tcc tgc ttt cac aga att att cca ggg ttt acg tgt Gly Tyr Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Thr Cys 75 80 85	652
cag agt ggt gac ttc aca cgc cat aca gca ttg gtg gca agt cca tct Gln Ser Gly Asp Phe Thr Arg His Thr Ala Leu Val Ala Ser Pro Ser 90 95 100	700
gca ggg aga aat ttg atg aca aga act tca tcc tga agca tacgggtcct Ala Gly Arg Asn Leu Met Thr Arg Thr Ser Ser * 105 110 115	750
ggcatcttgt ccatggcaaa tgctggaccc agcgtgaacg tttcccagtt ttttatctgc	810
cctgccaaga tgccaagaca gagtggttgg attgcaagca tgtggtcttt ggcaaggtga	870
aagatggcat gaatattgtg gaggtcatgg agcacttggg gtccaagaat ggcaagatca	930
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agttggcagc ggcaagcgcg ctgcggttcc ggtggcgcc atg tcg ttc tgc agc Met Ser Phe Cys Ser 1 5	174
ttc ttc ggg ggc gag gtt ttc cag aat cac ttt gaa cct ggc gtt tac Phe Phe Gly Gly Val Phe Gln Asn His Phe Glu Pro Gly Val Tyr 10 15 20	222

gtg tgt gcc Val Cys Ala	aag tgt g Lys Cys G 25	gc tat gag ly Tyr Glu	ctg ttc tcc Leu Phe Ser 30	agc cgc tcg aag tat Ser Arg Ser Lys Tyr 35	270
	Ser Pro T			acc att cac gcc gac Thr Ile His Ala Asp 50	318
agc gtg gcc Ser Val Ala 55	aag cgt c Lys Arg P	cg gag cac ro Glu His 60	aat aga tct Asn Arg Ser	gaa gcc ttg aag gtg Glu Ala Leu Lys Val 65	366
tcc tgt ggc Ser Cys Gly 70	Lys Cys G	gc aat ggg ly Asn Gly 75	ttg ggc cac Leu Gly His 80	gag ttc ctg aac gac Glu Phe Leu Asn Asp 85	414
ggc ccc aag Gly Pro Lys				attcagcag ctcgctgaag	465
tttgtcccta	aaggcaaaga	aacttctgco	c teceagggte	actaggcggg cagcccacac	525
ccaccccaga	cggccaccac	actgaggcca	a cacgttggcc	attccacctt ggagttggaa	585
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gccccggctc	tgaacaagac	cttttcgttt	cttggaaaag	agactcattt gctgatggtt	705
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cataactcta	accagcacag	ggctgaggco	tgcagtgcac	acctgcaggg aggcccttcc	1245
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		Leu					Ile								cag Gln	156
													aat Asn		tta Leu 45	204
		_	_			-	_				-	_	cct Pro			252
								_				_	gtg Val 75	_	_	300
													aag Lys			348
													ggg			396
													gaa Glu			444
									_		_	_	cta Leu		_	492
													agt Ser 155			540
								-	_		_	-	ttg Leu		_	588
													atg Met			636

175 180 185

	His		_		ttg Leu 195	_	_	_	Gly	_	_	act Thr 205	684
_		_	_		ata Ile			-		_	_		732
					gat Asp								780
_	-	_		_	aaa Lys	_	_	-	_	_		-	828
					ttt Phe								876
					gaa Glu 275								924
					tta Leu								972
					gca Ala								1020
					gca Ala								1068
					agt Ser								1116
					ggc Gly 355							act Thr 365	1164
					cct Pro								1212
					att Ile								1260
					gta Val								1308

						act Thr 420										1356
						ggc Gly										1404
						ctt Leu										1452
						tgt Cys										1500
						cga Arg										1548
						gac Asp 500										1596
						gaa Glu										1644
						aaa Lys										1692
						acc Thr										1740
						acg Thr										1788
						aga Arg 580						taa *	tcad	cagad	ect	1837
cago	ggct	cc a	acaç	gggag	ga aa	aaaa	caato	act	ggto	ttg	tcta	ataag	gtc a	actct	gcttt	1897
atct	tgct	aa a	agaca	aattt	t to	caago	caato	c ctt	tagt	ttt	agtt	ttct	gg a	aatag	gctagt	1957
atto	ggtt	ctt c	ctagt	tttt	it ca	acctt	ttag	y ttt	ttac	ctct	aatt	ttgt	caa d	ccato	gtatat	2017
gcta	ıgcaç	gtc o	cactt	ctad	cg co	cacca	accca	a aat	gggt	cag	acco	cttga	aag a	aaaco	gtcact	2077
tcaa	acto	cag a	aatga	aaatt	t to	catta	aatat	taa	aatt	gtg	aago	caaag	ggt (	caata	aggctt	2137
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			125					130					135		
	_			_										cgg Arg	785
														aga Arg	833
					aag Lys 175										881
					ctg Leu									_	929
_					tgt Cys						_		_		977
				-	gga Gly	_									1025
				_	gat Asp			_	_		_				1073
					cag Gln 255							_			1121
					agg Arg										1169
					ttc Phe										1217
		_	_		atc Ile		_			_		_		_	1265
					gct Ala										1313
					cct Pro 335			_					_		1361
					aac Asn										1409

aaa aca aat cca gaa gtc cat aat tac cag cct caa tat cat cct aat Lys Thr Asn Pro Glu Val His Asn Tyr Gln Pro Gln Tyr His Pro Asn 365 370 375	1457
atc cat ccc agc cag ccc cgg tgg cat cct cac tct cca aat gtc agg  Ile His Pro Ser Gln Pro Arg Trp His Pro His Ser Pro Asn Val Arg  380 385 390	1505
cca tcc ttt cag gat gac agg tcg cat tgg aaa gca tcg gcc agt gga Pro Ser Phe Gln Asp Asp Arg Ser His Trp Lys Ala Ser Ala Ser Gly 395 400 405	1553
gat gac agc cat ttt gat tat gtc cac gac cag aac cag aag aac tta Asp Asp Ser His Phe Asp Tyr Val His Asp Gln Asn Gln Lys Asn Leu 410 415 420	1601
gga ggg atg caa agt atg atg tat cga gat aaa ctc atg act gca ctt Gly Gly Met Gln Ser Met Met Tyr Arg Asp Lys Leu Met Thr Ala Leu 425 430 435 440	1649
tga gaga ctgaagcatc tctcttccat tcaccttcat agtttcattg cattccatga *	1706
aaagtgtctt ggcctcagat ggatggatgt gtttggacga gtgtctttaa ggagtagtcc	1766
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gagaggccca gtatttaggc gacagtgaat ttattactct gaagagggtt ctgcacatat

ttccaaatta tattggtggt catcagaagt aggtgatagg aagaaatact tctcaagggt

gcaaaa atg cag agt aat aaa act ttt aac ttg gag aag caa aac cat

Met Gln Ser Asn Lys Thr Phe Asn Leu Glu Lys Gln Asn His

1 5 10

act cca aga aag cat cat caa cat cac cac cag cag cac cac cag

Thr Pro Arg Lys His His Gln His His Gln Gln Gln His His Gln

cag caa cag cag cag ccg cca cca ccg cca ata cct gca aat ggg caa

384
Gln Gln Gln Gln Pro Pro Pro Pro Pro Ile Pro Ala Asn Gly Gln

35

40

45

cag gcc agc agc caa agt gtg tat atg cta gat gaa ggc ttg act att
Gln Ala Ser Ser Gln Ser Val Tyr Met Leu Asp Glu Gly Leu Thr Ile
50 55 60

gac ctg aag aat ttt aga aaa cca gga gag aag acc ttc acc caa cga 480 Asp Leu Lys Asn Phe Arg Lys Pro Gly Glu Lys Thr Phe Thr Gln Arg

		65	5				70	ס				75	5			
ago Sei	c cgt Arg 80	g Lei	ttt 1 Phe	gtg Val	g gga L Gly	a aat 7 Asn 85	Let	cct Pro	cco Pro	c gad o Asp	c ato 7 Ile 90	∃ Thi	gag Glu	g gaa 1 Glu	a gaa 1 Glu	528
ato Met 95	: Arc	g aaa g Lys	a cta s Leu	ttt Phe	gag Glu 100	Lys	tat Tyr	gga Gly	a aag ⁄ Lys	g gca s Ala 105	ı Gly	gaa Glu	a gto ı Val	tto Phe	att Ile 110	576
cat His	aag Lys	gat Asp	aaa Lys	gga Gly 115	<sup>r</sup> Phe	ggc Gly	ttt Phe	ato Ile	cgc Arg 120	r Leu	gaa Glu	acc Thr	cga Arg	aco Thr 125	cta Leu	624
gcg Ala	gag Glu	att Ile	gcc Ala 130	Lys	gtg Val	gag Glu	ctg Leu	gac Asp 135	Asn	atg Met	cca Pro	cto Leu	cgt Arg 140	Gly	aag Lys	672
cag Gln	ctg Leu	cgt Arg 145	Val	cgc Arg	ttt Phe	gcc Ala	tgc Cys 150	His	agt Ser	gca Ala	tcc Ser	Leu 155	Thr	gtt Val	cga Arg	720
aac Asn	ctt Leu 160	Pro	cag Gln	tat Tyr	gtg Val	tcc Ser 165	aac Asn	gaa Glu	ctg Leu	ctg Leu	gaa Glu 170	gaa Glu	gcc Ala	ttt Phe	tct Ser	768
gtg Val 175	ttt Phe	ggc	cag Gln	gta Val	gag Glu 180	agg Arg	gct Ala	gta Val	gtc Val	att Ile 185	gtg Val	gat Asp	gat Asp	cga Arg	gga Gly 190	816
agg Arg	ccc Pro	tca Ser	gga Gly	aaa Lys 195	ggc Gly	att Ile	gtt Val	gag Glu	ttc Phe 200	tca Ser	ggg	aag Lys	cca Pro	gct Ala 205	gct Ala	864
cgg Arg	aaa Lys	gct Ala	ctg Leu 210	gac Asp	aga Arg	tgc Cys	agt Ser	gaa Glu 215	ggc Gly	tcc Ser	ttc Phe	ctg Leu	cta Leu 220	acc Thr	aca Thr	912
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gaa Glu 255	cga Arg	gag Glu	cag Gln	cca Pro	ccc Pro 260	aga Arg	ttt Phe	gca Ala	cag Gln	cct Pro 265	ggc Gly	tcc Ser	ttt Phe	gag Glu	tat Tyr 270	1056
gaa Glu	tat Tyr	gcc Ala	atg Met	cgc Arg 275	tgg Trp	aag Lys	gca Ala	ctc Leu	att Ile 280	gag Glu	atg Met	gag Glu	aag Lys	cag Gln 285	cag Gln	1104
cag Gln	gac Asp	caa Gln	gtg Val 290	gac Asp	cgc Arg	aac Asn	Ile	aag Lys 295	gag Glu	gct Ala	cgt Arg	gag Glu	aag Lys 300	ctg Leu	gag Glu	1152

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cag Gln	gat Asp 320	ttg Leu	atg Met	agg Arg	cgc Arg	caa Gln 325	gaa Glu	gaa Glu	ctt Leu	cgg Arg	agg Arg 330	atg Met	gaa Glu	gag Glu	ctg Leu	1248
cac His 335	aac Asn	caa Gln	gag Glu	gtg Val	caa Gln 340	aaa Lys	cga Arg	aag Lys	caa Gln	ctg Leu 345	gag Glu	ctc Leu	agg Arg	cag Gln	gag Glu 350	1296
														gaa Glu 365		1344
														gat Asp		1392
														gct Ala		1440
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														act Thr		1536
														aca Thr 445		1584
														cgt Arg		1632
					ttt Phe									taa *	taa	1680
gtt	gcagt	gt d	ctagi	ttc	c aa	aaaco	cctta	a aaa	agaag	ggac	cctt	tttg	gga d	ctago	ccagaa	1740
ttc	cacco	ctg (	gaaaa	agtgi	it ag	gggat	tcct	t tc	caata	agtt	agat	ctac	ccc t	gcct	gtact	1800
acto	ctago	gga g	gtate	gctg	ga gg	gcaga	agggo	c aag	gggag	aaaa	tggt	tatta	aaa o	caagt	caatt	1860
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gag ggc tgg Glu Gly Trp 180	Pro Ala Pr					632
gca gag gac Ala Glu Asp 195						680
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<220>

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gctactctcc gggaggggcg cttcccgacg ccaagacaaa agg atg cca cgg aga Met Pro Arg Arg

_			-		-	gtc Val		-				_		_	_	223
						tct Ser										271
	-	_				ata Ile		_	-	-	-				_	319
_	_			_		aaa Lys	_	_								367
_	_	_	_		_	aaa Lys 75		_	_	_		-	_	_	_	415
	_	_	-			atg Met	_		-	_	_					463
	-	_			-	gag Glu			_			-			-	511
						cct Pro										559
	-	_			_	tct Ser		-				_				607
_					-	ggc Gly 155			-	-	-				_	655
						agt Ser	_				-		-	-		703
						gaa Glu										751
						cag Gln										799
aac Asn	Val					aga Arg										847
cag	tgt	ggg	aag	cca	cag	gaa	agt	act	ggg	agg	ggt	tct	gct	ttt	ctc	895

G	ln	Cys 230	Gly	Lys	Pro	Gln	G1u 235	Ser	Thr	Gly	Arg	Gly 240	Ser	Ala	Phe	Leu	
I				cag Gln													943
		_	_	gcc Ala				-	_								991
				att Ile 280			-		-		_	-			_		1039
				att Ile													1087
	_	-	_	agg Arg	_									_			1135
L			-	cct Pro			_		_		-	_					1183
	_	-	-	gag Glu			_	-			-	-	-		-	-	1231
				gag Glu 360													1279
		-	_	ttc Phe	_	-	_				_	_					1327
				gaa Glu													1375
I				gaa Glu													1423
				gct Ala													1471
				gaa Glu 440													1519
				ttt Phe													1567

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gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg aca cgg Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg Thr Arg 695 700 705	2287
acc aaa gct ggc aga gga aga agg aga aaa ttc tga attt ctagggtcca Thr Lys Ala Gly Arg Gly Arg Arg Lys Phe * 710 715 720	2337
aaagttgaca aaaccattag taggaggggt gggccatgtt cattaagcca tagtggtccc	2397
tagttcattg ttgagcaagt tttagccctg cagttttcac caccagcacc tacccagcat	2457
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	120
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ccgctactct ccgggagggg cgcttcccga cgccaagaca aaaggatgcc acggagaaag	240
aaaaaagtta aagaagtctc cgaatctcgg aacctggaga agaaggatgt ggaaactacc	300
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aatagagcaa agtgtttggc caaaagaaaa atcgcacaga tgacagaaga agaacagttt	480
gctctggctc tcaaaatgag tgagcaggaa gctagggagg tgaacagcca ggaggaggaa	540
gaagaggagc tcttgaggaa agccattgct gaaagcctga atagttgccg gccttctg atg ctt ccg cta cca gat ctc gac ctc tgg cca ctg gac cgt ctt ccc Met Leu Pro Leu Pro Asp Leu Asp Leu Trp Pro Leu Asp Arg Leu Pro 1 5 10 15	598 646
agt ccc atc aag aga aaa cca cag act ctg ggc tca ctg aag tct tcc Ser Pro Ile Lys Arg Lys Pro Gln Thr Leu Gly Ser Leu Lys Ser Ser 20 25 30	694

						act Thr									gct Ala	742
						ttg Leu 55										790
		_		-	_	gaa Glu			-	-				_		838
_						gac Asp		_	_	-	_				_	886
				_		gtc Val	_			_	_	_	_		_	934
		_	_	_	-	gag Glu	-	-	-	-						982
	-		_	_		tgc Cys 135	_		_	_		-				1030
						gcc Ala										1078
		_	_			aga Arg					_		_	_	-	1126
			-	_	_	act Thr			-		_	_			-	1174
						ctg Leu										1222
						ctt Leu 215										1270
						tgt Cys										1318
						gaa Glu										1366
agt	ttc	ttg	gaa	cag	tct	gag	cac	aag	act	tca	gat	gca	gac	atc	aag	1414

Ser Phe Leu Glu Gln Ser Glu His Lys Thr Ser Asp Ala Asp Ile Lys 260 265 270	
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gca ggc tgc agc aga gag atg cag agt tct ttc aca cgt cgt gac tta Ala Gly Cys Ser Arg Glu Met Gln Ser Ser Phe Thr Arg Arg Asp Leu 290 295 300	1510
aat gaa tot occ gto aag tot ttt gtt too att toa gaa goo aca gat Asn Glu Ser Pro Val Lys Ser Phe Val Ser Ile Ser Glu Ala Thr Asp 305 310 315 320	1558
tgc tta gtg gac ttt aaa aag caa gtt act gtc cag cca ggt agt cgg Cys Leu Val Asp Phe Lys Lys Gln Val Thr Val Gln Pro Gly Ser Arg 325 330 335	1606
aca cgg acc aaa gct ggc aga gga aga agg aga aaa ttc tga atttcta Thr Arg Thr Lys Ala Gly Arg Gly Arg Arg Arg Lys Phe * 340 345 350	1655
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		_	acg Thr	_			-									279
			caa Gln													327
_		_	aaa Lys	_		_					_			~	~ ~	375
			aga Arg 60													423
			tgg Trp													471
			aca Thr													519
			ggc Gly													567
			ctc Leu													615
			cgg Arg 140		_					_	_	_			tga *	663
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aggg	gaag	igc o	cctgg	ratto	t ca	ctca	tgtg	r aga	tctt	gaa	tctc	tttc	tt t	gtto	tgttt	843
gttt	agtt	ag t	tatca	tctg	ıg ta	aaat	agtt	aaa	aaac	aac	aaaa	aact	ct g	gtato	tgttt	903
ctag	catg	tg d	ctgca	ıttga	c to	tatt	aato	aca	tttc	aaa	ttca	ccct	ac a	attco	tctcc	963
tctt	cact	ag d	cctct	ctga	a gg	tgtc	ctgg	сса	gccc	tgg	agaa	ıgcac	tg g	gtgtc	tgcag	1023
cacc	cctc	ag t	tcct	gtgc	c to	agcc	caca	ggc	cact	gtg	ataa	tggt	ct g	gttta	ıgcact	1083
tctg	tatt	ta t	tgta	agaa	ıt ga	ttat	aatg	aag	atac	aca	ctgt	aact	ac a	agaa	attat	1143
aaat	gttt	tt d	cacat	cagg	rc tg	ttct	tttt	ttt	tttt	tgg	aggo	gagg	rtt a	aagc	attac	1203
tatt	tgca	aa g	gcact	ctgt	a go	tccc	tgtt	atg	ggga	tag	gtaa	ctaa	itc a	gaat	aataa	1263

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act gaa gtg gtt ctc ctt gct tgt ggt tca ttc aat ccc atc acc aac 160

Thr	Glu	Val	Val 10		Leu	Ala	Cys	Gly 15	Ser	Phe	. Asn	Pro	Ile 20		Asn	
								Ala					Asn		aca Thr	208
												Val			gcc Ala	256
											Arg				gca Ala 70	304
					aat Asn										gaa Glu	352
					tgg Trp											400
					gct Ala											448
					gga Gly											496
					tcc Ser 140											544
					gly ggg											592
aat Asn	ttg Leu	tgg Trp	aag Lys 170	agt Ser	gaa Glu	gac Asp	atc Ile	acc Thr 175	caa Gln	atc Ile	gtg Val	gcc Ala	aac Asn 180	tat Tyr	ggg ggg	640
					cgg Arg											688
					tgg Trp											736
gaa Glu 215					gac Asp 220											784
aga Arg																832

				235					240					245		
														agg Arg		880
														gct Ala		928
aca Thr		gaat	ttcta	aca (	gcato	gatai	tt to	caga	cttco	c cat	tttg	ggga	tct	gaaa	caa	984
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gtt																1047
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														gac Asp		99
														ggt Gly		147
														gcc Ala 55		195
_			-											aaa Lys		243
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90	95		100	
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			gag ttt gtc aat att Glu Phe Val Asn Ile 20	219
			cta acc agg ctg tat Leu Thr Arg Leu Tyr 40	267
			gct gtt tca ggg ctg Ala Val Ser Gly Leu 55	315
		-	tct agt gag ttc cag Ser Ser Glu Phe Gln 70	363
			caa gca act cag tcc Gln Ala Thr Gln Ser 85	411
		Ser Gly Thr V	gtg aag ttt gat gga Val Lys Phe Asp Gly 100	459

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act ccc aac aat act gtg tgg aag att gca agt gat tgc ttc cgt ttt Thr Pro Asn Asn Thr Val Trp Lys Ile Ala Ser Asp Cys Phe Arg Phe 125 130 135	555
caa gat tgg tct agt agt taa ag gggcaaaagt ccattctcat ttggtccatt Gln Asp Trp Ser Ser * 140	608
agttccagca attgaaattt atgtgaatta ttttgattgt agaagcacta taatatgtgc	668
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cactaatgac attettataa taatattaaa cacatgatet tggtactaac atacteactg	848
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caatataaca ctctgggaag aagtggagtt ttttggttat taggttaatt ttctagtaaa	968
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<213> Homo sapiens

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ata aca gtg att caa ata ttt cat tca gat tta cct atg cct aat gaa 333 Ile Thr Val Ile Gln Ile Phe His Ser Asp Leu Pro Met Pro Asn Glu 20 25 30

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				tct Ser									621
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				gct Ala									717
				tat Tyr									765
				aaa Lys 185									813
				gat Asp									861
				gag Glu									909
				aat Asn									957
				cgt Arg									1005
				ata Ile 265			_		-				1053

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gaggaattta ataattatga ttgttataaa taattatgta taattataat ctagggtaga	a 2339
aaatttagtt atttcattaa atttggacta gtgacaaaga ctgcaggtaa tgagaagcc	2399
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<sup>&</sup>lt;211> 2166

<sup>&</sup>lt;212> DNA

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gad Asp	ago Ser	tto Phe 25	e Leu	ctg Leu	g ctg Leu	g cag u Glr	g cag Gln 30	Ser	gtg Val	acg Thr	r ctg	g ggc ı Gly 35	Ser	tcg Ser	Gly Ggc	210
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cgt ctg ggt agc ggc tcc tcc gcc tcg gtg tat cgg gtt cgc tgc tgc Arg Leu Gly Ser Gly Ser Ser Ala Ser Val Tyr Arg Val Arg Cys Cys 30 35 40	207
ggc aac cct ggc tcg ccc ccc ggc gcc ctc aag cag ttc ttg ccg cca Gly Asn Pro Gly Ser Pro Pro Gly Ala Leu Lys Gln Phe Leu Pro Pro 45 50 55	255
gga acc acc ggg gct gcg gcc tct gcc gcc gag tat ggt ttc cgc aaa Gly Thr Thr Gly Ala Ala Ala Ser Ala Ala Glu Tyr Gly Phe Arg Lys 60 65 70 75	303
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ttg tat gga gtg ttt aca atc cac ttt tct cca aat gtg cca tca cgc Leu Tyr Gly Val Phe Thr Ile His Phe Ser Pro Asn Val Pro Ser Arg 95 100 105	399
tgt ctg ttg ctt gaa ctc ctg gat gtc agt gtt tcg gaa ttg ctc tta Cys Leu Leu Leu Glu Leu Leu Asp Val Ser Val Ser Glu Leu Leu Leu 110 115 120	447
tat tcc agt cac cag ggt tgt tcc atg tgg atg ata cag cat tgc gcc Tyr Ser Ser His Gln Gly Cys Ser Met Trp Met Ile Gln His Cys Ala 125 130 135	495
cga gat gtt ttg gag gcc ctt gct ttt ctt cat cat gag ggc tat gtc Arg Asp Val Leu Glu Ala Leu Ala Phe Leu His His Glu Gly Tyr Val 140 145 150 155	543
cat gcg gac ctc aaa cca cgt aac ata ttg tgg agt gca gag aat gaa	591

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-	_				cca Pro			_	-	_			_	_	_	1071
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					aaa Lys											1167
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gaacgcctgc	aagcc atg atg acc cac Met Met Thr His	ctg cat gtg aag tct a Leu His Val Lys Ser T	ca gaa ccc 351 hr Glu Pro

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	-	_		-		ttg Leu		Leu	_		-	_				399
_			_		_	tct Ser 35		_	_						_	447
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			-	-	His	acg Thr										543
						att Ile										591
			_		-	gaa Glu	-	_						_		639
			_	•		ctc Leu 115	_			_	_	_				687
						ttc Phe		_	_		-			-	•	735
					_	aat Asn	_		_				_			783
	_		-		-	gaa Glu		-			-	_				831
_	_	_	_			aaa Lys	_				_		_	~ ~		879
						atg Met 195	_	-	-		-		_			927
						gct Ala										975
						gga Gly										1023

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gta Val	cac His 270	gtc Val	aaa Lys	gaa Glu	gag Glu	ccc Pro 275	ctc Leu	gat Asp	cca Pro	gag Glu	gaa Glu 280	gct Ala	gaa Glu	ggg Gly	ccc Pro	1167
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tct Ser	gat Asp	gac Asp 1	atg ( Met :	aag Lys :	aag Lys :	ctg Leu i	aag Lys . 15	gcc Ala	cga Arg	atg ( Met 1	cac His	cag Gln 20	gcc Ala	ata Ile	gaa Glu	159
aga Arg	ttt Phe 25	tat ( Tyr /	gat a Asp 1	aaa a Lys 1	atg ( Met (	caa Gln 30	aat ( Asn )	gca Ala	gaa Glu	tca ( Ser (	gga Gly 35	cgt ( Arg (	gga ( Gly (	cag ( Gln '	gtg Val	207
atg Met 40	tcg . Ser :	agc ( Ser 1	ctg g Leu <i>l</i>	gca ( Ala (	gag o Glu 1 45	ctg ( Leu (	gag ( Glu /	gac Asp	gac Asp	ttc a Phe 1 50	aaa Lys	gag ( Glu (	ggc ( Gly (	tac ( Tyr 1	ctg Leu 55	255
gag a Glu '	aca ( Thr	gtg ( Val <i>l</i>	gcg ( Ala <i>l</i>	gct ( Ala 7 60	tat ( Tyr 1	tat ( Tyr (	gag ( Glu (	gag ( Glu (	cag ( Gln 1 65	cac d His I	cca ( Pro (	gag ( Glu 1	ctc a Leu :	act o Thr 1	cct Pro	303

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														cag Gln			197
_	_	-	_	-	_		-		-				_	agg Arg 70			245
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		10> 11> C 12> (		(8	64)												
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actt	ttta	itt c	tact	atgt	a ta	tgta	tgga	ata	gtat	taa	taaa	tgaa	ct a	ıggga	aggat	•	120

Met Glu Thr Thr Leu Leu

174

222

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	_	_	_		aaa Lys	_		_		_				_		318
					gac Asp 60											366
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				-	ttc Phe	_	_	_			-				_	510
					aaa Lys											558
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														aat Asn 90		469
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_												atc Ile 375			_	1274
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					gag Glu					788
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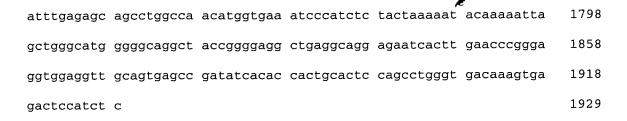
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120

444

492

125

gca ctc cga ggt cat ctg gag gtt gtc aag ttt ttg att cag tgt gac

Ala Leu Arg Gly His Leu Glu Val Val Lys Phe Leu Ile Gln Cys Asp

tgg acg atg gcc ggc cag cag gaa gta ttt aag aag agc cat gcc Trp Thr Met Ala Gly Gln Gln Gln Gly Val Phe Lys Lys Ser His Ala

130 135 140

540

atc caa cag gcc ctc att gct gca gcc agc atg ggt tat act gag gta

Ile Gln Gln Ala Leu I 145		Ala Ser Met 150	Gly Tyr Th		
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Met Phe Asp Glu Ala Ser Ala

1 5

atc act tcc tac gag aag ttt cta acc ccc gag gag ccc ttt cca ctc 159
Ile Thr Ser Tyr Glu Lys Phe Leu Thr Pro Glu Glu Pro Phe Pro Leu

15

ctg gga cct cct cgc ggg gtg ggc acc tgc ccg agc gag gag ccg ggc 207 Leu Gly Pro Pro Arg Gly Val Gly Thr Cys Pro Ser Glu Glu Pro Gly

346

		Leu										Ser				cgc Arg 55	255
						cgc Arg					Arg						303
						gcc Ala										tca Ser	351
						gat Asp											399
						ttt Phe											447
						att Ile 125											495
						cca Pro											543
						ccc Pro											591
Last Sant Man	aaa Lys	aag Lys	aaa Lys 170	aac Asn	aag Lys	cac His	cgg Arg	aat Asn 175	tta Leu	gat Asp	gaa Glu	ctc Leu	cct Pro 180	tgg Trp	agt Ser	gca Ala	639
						cag Gln											687
	gtg Val 200	agt Ser	act Thr	gag Glu	atg Met	ggt Gly 205	ctt Leu	cgg Arg	gag Glu	caa Gln	ctt Leu 210	gat Asp	att Ile	att Ile	aag Lys	atc Ile 215	735
	att Ile	gat Asp	cct Pro	tct Ser	gct Ala 220	cag Gln	atc Ile	tcc Ser	cct Pro	aca Thr 225	gac Asp	agg Arg	gag Glu	ttt Phe	att Ile 230	att Ile	783
	gaa Glu	ctt Leu	Asn	tgt Cys 235	ctc Leu	aca Thr	gat Asp	Glu	aaa Lys 240	ctg Leu	aag Lys	cag Gln	gtc Val	aga Arg 245	aac Asn	tat Tyr	831
						cct Pro	Arg										879

										gga Gly						927
										gtc Val 290						975
										aac Asn						1023
										gca Ala						1071
		~			_	_		_	-	cgg Arg						1119
										agg Arg						1167
										gtg Val 370						1215
										gtt Val			taa *	taaç	gggt	1264
gaat	ttat	cca a	acgtt	cttt	g to	gagca	attaa	a aat	acto	ccat	cctt	atgg	ggt t	taca	atgcaa	1324
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gatgcaggaa ttcatctaat tttcactgcc gggcgaggtg tgagagccct agcatctgaa 180
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	_	-	-	_	_	-	_				_	-	aag Lys			424
													ttt Phe			472
													atc Ile			520
													tac Tyr 120			568
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cgt Arg	aat Asn	ctt Leu	gga Gly	ctt Leu 175	act Thr	cca Pro	atg Met	gat Asp	caa Gln 180	gga Gly	tca Ser	ctc Leu	atg Met	gca Ala 185	gcc Ala	760
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Pro	Phe	Tyr 205	Leu	Ser	Ala	Val	Leu 210	Cys	Val	Phe	Leu	Phe 215	ttc Phe	Tyr	Cys	856
gtt Val	ata Ile	aga Arg	gac Asp	gta Val	atc Ile	tac Tyr	cct Pro	tat Tyr	gtt Val	tat Tyr	gaa Glu	aag Lys	aaa Lys	gat Asp	aat Asn	904

220 225 230

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		_		cga Arg					_	_			-		1048
-			_	ctt Leu	_	_	_	_			_	_	-	_	1096
				cat His											1144
	_	_		aga Arg 320	_					-		_	-		1192
_	_			cca Pro		_				_			_	_	1240
				gga Gly						_		-		_	1288
				cca Pro									_		1336
_		-	_	tcc Ser		_			_		_		_	_	1384
_			_	gtg Val 400				_	-			_			1432
	_			ctt Leu		-	-								1480
_			_	gtg Val		-		~			_		_	_	1528
				agg Arg											1576

cac tag aaaaagcatt gaatggaaaa tcaatattta aaacaaagtt caatttagct His * 460	1632
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gga agc ccc tgg cca ggc ctg cct ctc ccc tcc ctg gtg ggc cca gcg	395

Gly Ser Pro Trp Pro Gly Leu Pro Leu Pro Ser Leu Val Gly Pro Ala

		Leu	tgc Cys			Leu			Ala	4	443
			gag Glu		Gly					4	191
			gcc Ala							5	539
			acc Thr 85							5	87
			ctc Leu							$\epsilon$	35
			tgg Trp							6	83
			acg Thr							7	31
			ggg Gly							7	79
			gtc Val 165							8	27
			gtg Val							8	75
			gcc Ala							9	23
			cac His							9	71
			gtg Val							10	19
		Val	tgc Cys 245							10	67

						Ala									caa Gln 270	1115
						caa Gln				-		_	_			1163
					-	cag Gln	-	_		_	_					1211
						acg Thr										1259
						tgc Cys 325										1307
						agc Ser										1355
						ccc Pro										1403
						cag Gln										1451
						ttc Phe										1499
						gac Asp 405										1547
						cac His										1595
						ccc Pro										1643
		Val				agc Ser										1691
						agg Arg										1739
gac	gcc	gtg	cac	aac	ttc	gcc	gac	ggg	ctg	gcc	gtg	ggc	gcc	gcc	ttc	1787

Asp Ala Val His Asn Phe Ala Asp Gly Leu Ala Val Gly Ala Ala Phe 480 485 490	
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gag agc gag gcc tgg atc ctg gca gtg gcc acc ggc ctg ttc ctc tac Glu Ser Glu Ala Trp Ile Leu Ala Val Ala Thr Gly Leu Phe Leu Tyr 560 565 570	2027
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<220>

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ccg	geggg	gctg	ggad										g Ly		t gac .a Asp		171
aag Lys	g gag Glu	tcg Ser 15	Arg	pro	gag Glu	aac Asn	gag Glu 20	ı Glu	gag Glu	g cgg L Arg	cca Pro	a aag Lys 25	Gln	tac Tyr	agc Ser		219
tgg Trp	gat Asp 30	Gln	g cgc Arg	gag Glu	, aag Lys	gtt Val 35	Asp	cca Pro	aaa Lys	gac Asp	tac Tyr 40	Met	ttc Phe	agt Ser	gga Gly		267
ctg Leu 45	Lys	gat Asp	gaa Glu	aca Thr	gta Val 50	Gly	cgc Arg	tta Leu	cct Pro	ggg Gly 55	Thr	gta Val	gca Ala	gga Gly	caa Gln 60		315
cag Gln	ttt Phe	ctc Leu	att Ile	caa Gln 65		tgt Cys	gag Glu	aac Asn	tgt Cys 70	Asn	atc Ile	tat Tyr	att Ile	ttt Phe 75	gat Asp		363
cac His	tct Ser	gct Ala	aca Thr 80	Val	acc Thr	att Ile	gat Asp	gac Asp 85	tgt Cys	act Thr	aac Asn	tgc Cys	ata Ile 90	att Ile	ttt Phe		411
ctg Leu	gga Gly	ccc Pro 95	gtg Val	aaa Lys	ggc Gly	agc Ser	gtg Val 100	ttt Phe	ttc Phe	cgg Arg	aat Asn	tgc Cys 105	aga Arg	gat Asp	tgc Cys		459
aag Lys	tgc Cys 110	aca Thr	tta Leu	gcc Ala	tgc Cys	caa Gln 115	caa Gln	ttt Phe	cgt Arg	gtg Val	cga Arg 120	gat Asp	tgt Cys	aga Arg	aag Lys		507
ctg Leu 125	gaa Glu	gtc Val	ttt Phe	ttg Leu	tgt Cys 130	tgt Cys	gcc Ala	act Thr	caa Gln	ccc Pro 135	atc Ile	att Ile	gag Glu	tct Ser	tcc Ser 140		555
tca Ser	aat Asn	atc Ile	aaa Lys	ttt Phe 145	gga Gly	tgt Cys	ttt Phe	caa Gln	tgg Trp 150	tac Tyr	tat Tyr	cct Pro	gaa Glu	tta Leu 155	gct Ala		603
ttc Phe	cag Gln	ttc Phe	aaa Lys 160	gat Asp	gca Ala	ggg Gly	cta Leu	agt Ser 165	atc Ile	ttc Phe	gac Asp	aat Asn	aca Thr 170	tgg Trp	agt Ser		651
aac Asn	att Ile	cat His 175	gac Asp	ttt Phe	aca Thr	cct Pro	gtg Val 180	tca Ser	gga Gly	gaa Glu	ctc Leu	aac Asn 185	tgg Trp	agc Ser	ctt Leu		699
ctt Leu	cca Pro 190	gaa Glu	gat Asp	gct Ala	gtg Val	gtt Val 195	cag Gln	gac Asp	tat Tyr	gtt Val	cct Pro 200	ata Ile	cct Pro	act Thr	acc Thr		747
gaa Glu	gag Glu	ctc Leu	aaa Lys	gct Ala	gtt Val	cgt Arg	gtt Val	tcc Ser	aca Thr	gaa Glu	gcc Ala	aat Asn	aga Arg	agc Ser	att Ile		795

205 210	215 220	
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cta att gat gag atg gtt ggt aaa gg Leu Ile Asp Glu Met Val Gly Lys Gl 255 260	gc ttt ttc cta gtt cag aca aag 9 y Phe Phe Leu Val Gln Thr Lys 265	39
gaa gtg tcc atg aaa gct gag gat gc Glu Val Ser Met Lys Ala Glu Asp Al 270 275		87
gca cct gac ttc ctt cct ctt ctg aa Ala Pro Asp Phe Leu Pro Leu Leu As 285	c aaa ggt cct gtt att gcc ttg 10. n Lys Gly Pro Val Ile Ala Leu 295 300	35
gag ttt aat ggg gat ggt gct gta ga Glu Phe Asn Gly Asp Gly Ala Val Gl 305		83
gag ata ttc aat ggg acc aag atg tt Glu Ile Phe Asn Gly Thr Lys Met Pho 320	e Val Ser Glu Ser Lys Glu Thr	31
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aag cag aat tta gaa gaa cag ttg gat aga ctc atg caa caa tta caa Lys Gln Asn Leu Glu Gln Leu Asp Arg Leu Met Gln Gln Leu Gln 15 20 25	339
gat ctg gag gaa tgc aga gag gaa ctt gat aca gat gaa tat gaa gaa Asp Leu Glu Glu Cys Arg Glu Glu Leu Asp Thr Asp Glu Tyr Glu Glu 30 35 40	387
acc aaa aag gaa act ctg gag caa cta agt gaa ttt aat gat tca cta Thr Lys Lys Glu Thr Leu Glu Gln Leu Ser Glu Phe Asn Asp Ser Leu 45 50 55 60	435
aag aaa att atg tct gga aat atg act ttg gta gat gaa cta agt gga Lys Lys Ile Met Ser Gly Asn Met Thr Leu Val Asp Glu Leu Ser Gly 65 70 75	483
atg cag ctg gct att cag gca gct atc agc cag gcc ttt aaa acc cca Met Gln Leu Ala Ile Gln Ala Ala Ile Ser Gln Ala Phe Lys Thr Pro 80 85 90	531
gag gtc atc aga ttg ttt gca aag aaa caa cca ggt cag ctt cgg aca Glu Val Ile Arg Leu Phe Ala Lys Lys Gln Pro Gly Gln Leu Arg Thr 95 100 105	579
agg tta gca gag atg gat aga gat ctg atg gta gga aag ctg gaa aga Arg Leu Ala Glu Met Asp Arg Asp Leu Met Val Gly Lys Leu Glu Arg 110 115 120	627
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ctt gga gag aag ctg act gca gat gat gag gcc ttc ttg tca gca aat Leu Gly Glu Lys Leu Thr Ala Asp Asp Glu Ala Phe Leu Ser Ala Asn 145 150 155	723
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cgg ccc cca agt tac atg aac tac ctg cta gac tca cac ccc agc aaa Arg Pro Pro Ser Tyr Met Asn Tyr Leu Leu Asp Ser His Pro Ser Lys 175 180 185	819
aat att gat gtc ccc agc aag att agc ttc ctg tta aag atc cag gac Asn Ile Asp Val Pro Ser Lys Ile Ser Phe Leu Leu Lys Ile Gln Asp 190 195 200	867
ctg tga atacatgcgt aactgcaaga atggaagcaa aggatgaacc caagttaaag Leu * 205	923
cccagcacaa gaatatgatg taagcgcttt tgggaaatgc agagattttc ttttctcttc	983

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	<2	20> 21> 22>	CDS (1).	. (81	9)											
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gaa Glu	gaa Glu	gcg Ala 35	gcc Ala	tgt Cys	ggc Gly	agc Ser	aag Lys 40	aag Lys	cgg Arg	gta Val	gtg Val	cca Pro 45	ggt Gly	att Ile	gtg Val	144
tac Tyr	ctg Leu 50	ggc Gly	cat His	atc Ile	ccg Pro	ccg Pro 55	cgc Arg	ttc Phe	cgg Arg	ccc Pro	ctg Leu 60	cac His	gtc Val	cgc Arg	aac Asn	192
ctt Leu 65	ctc Leu	agc Ser	gcc Ala	tat Tyr	ggc Gly 70	gag Glu	gtc Val	gga Gly	cgc Arg	gtc Val 75	ttc Phe	ttt Phe	cag Gln	gct Ala	gag Glu 80	240
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aaa Lys	aag Lys	cgg Arg	tcc Ser 100	tac Tyr	acc Thr	aag Lys	gac Asp	tac Tyr 105	acc Thr	gag Glu	gga Gly	tgg Trp	gtg Val 110	gag Glu	ttc Phe	336
														aac Asn		384
cct Pro	atg Met 130	ggt Gly	gcc Ala	cgc Arg	agg Arg	cgc Arg 135	agc Ser	ccc Pro	ttc Phe	cgt Arg	tat Tyr 140	gat Asp	ctt Leu	tgg Trp	aac Asn	432
ctc Leu 145	aag Lys	tac Tyr	ttg Leu	cac His	cgt Arg 150	ttc Phe	acc Thr	tgg Trp	tcc Ser	cac His 155	ctc Leu	agc Ser	gag Glu	cac His	ctc Leu 160	480
gcc	ttt	gag	cgc	cag	gtg	cgc	agg	cag	cgc	ttg	aga	gcg	gag	gtt	gct	528

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tgg aca ttt gcc cag cgt cct act gag cag gaa ctg agg gcc cgt aaa Trp Thr Phe Ala Gln Arg Pro Thr Glu Gln Glu Leu Arg Ala Arg Lys 210 215 220	672
gca gca cgg cca ggg gga cgt gaa cgg gct cgc ctg gca act gcc cag Ala Ala Arg Pro Gly Gly Arg Glu Arg Ala Arg Leu Ala Thr Ala Gln 225 230 235 240	720
gac aag gcc cgc tcc aac aaa ggg ctc ctg gcc agg atc ttt gga gcc Asp Lys Ala Arg Ser Asn Lys Gly Leu Leu Ala Arg Ile Phe Gly Ala 245 250 255	768
ccg cca ccc tca gag agc atg gag gga cct tcc ctt gtc agg gac tcc Pro Pro Pro Ser Glu Ser Met Glu Gly Pro Ser Leu Val Arg Asp Ser 260 265 270	816
tga gggc ctgggtggcc ccttccattt cctggccctg ctctgcttcc tgtctacctc *	873
atactagaat gatcgtgact acccgggcag acattttact gtgtttctca gaccaagtgt	933
ctactgatgg cccaaacatg gagttttgtg ggcttccact gtccccactc cgaactcctg	993
tatgtgcctg gctgagtcac ctaattcata ctgtcatact agcataatta tgactattgc	1053
atatgcttgt tttgtttgac tcttggctgc ctacgtctgt agggtcccct gaaaatccca	
	1113
cttcctgccc ccagaaaggg cctttatttc caactaggag gataatgcct agtccaggca	1113 1173
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	1173
atctttctct gtttagcagt cacaggtgag ggtggtatta gcatcttttt tatgtagaaa	1173 1233
atctttctct gtttagcagt cacaggtgag ggtggtatta gcatctttt tatgtagaaa aaattgagtt aatggggtgg actgggttgg gaagaaatac atttcctaat gtatttatag	1173 1233 1293
atcttctct gtttagcagt cacaggtgag ggtggtatta gcatctttt tatgtagaaa aaattgagtt aatggggtgg actgggttgg gaagaaatac atttcctaat gtatttatag aaaataaaaa tatttttatg tgcctttta ttttgttgg tggggaggtc attggacaag	<ul><li>1173</li><li>1233</li><li>1293</li><li>1353</li></ul>
atcttctct gtttagcagt cacaggtgag ggtggtatta gcatctttt tatgtagaaa aaattgagtt aatggggtgg actgggttgg gaagaaatac atttcctaat gtatttatag aaaataaaaa tatttttatg tgcctttta ttttgttgg tggggaggtc attggacaag ttccaacttt catcttgtgt tcccttcacc ttcatatcct gatcttagag ccccctccc	1173 1233 1293 1353 1413

<210> 157

<211> 1642 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (228)..(911) <400> 157 aaggateett aattaaatta ateeeceee eeceeegag tageggeage ggegaegaeg 60 gcggcggcag cgctccaact ggctcctcgc tccgggctcc gccgtcgagc cgggagagag 120 cctccgccag cggccaggca ccagccagac gacgccagcg accccggcct ctcggcggca 180 ccgcgctaac tcaggggctg cataggcacc cagagccgaa ctccaag atg gga ggc 236 Met Gly Gly aag ctc agc aag aag aag ggc tac aat gtg aac gac gag aaa gcc 284 Lys Leu Ser Lys Lys Lys Gly Tyr Asn Val Asn Asp Glu Lys Ala 332 Lys Glu Lys Asp Lys Lys Ala Glu Gly Ala Ala Thr Glu Glu Gly acc ccg aag gag agt gag ccc cag gcg gcc gca gag ccc gcc gag gcc 380 Thr Pro Lys Glu Ser Glu Pro Gln Ala Ala Glu Pro Ala Glu Ala 40 aag gag ggc aag gag aag ccc gac cag gac gcc gag ggc aag gcc gag 428 Lys Glu Gly Lys Glu Lys Pro Asp Gln Asp Ala Glu Gly Lys Ala Glu 60 gag aag gag ggc gag aag gac gcg gct gcc aag gag gac gcg 476 Glu Lys Glu Gly Glu Lys Asp Ala Ala Ala Lys Glu Glu Ala Pro 70 aag gcg gag ccc gag aag acg gag ggc gcg gca gag gcc aag gct gag 524 Lys Ala Glu Pro Glu Lys Thr Glu Gly Ala Ala Glu Ala Lys Ala Glu 85 572 Pro Pro Lys Ala Pro Glu Gln Glu Gln Ala Ala Pro Gly Pro Ala Ala 100 ggc ggc gag gcc ccc aaa gct gct gag gcc gcg gcc ccg gcc gag 620 Gly Gly Glu Ala Pro Lys Ala Ala Glu Ala Ala Ala Ala Pro Ala Glu 120 age geg gec cet gee geg gag gag cee age aag gag gaa ggg gaa 668 Ser Ala Ala Pro Ala Ala Gly Glu Glu Pro Ser Lys Glu Glu Gly Glu 135 140

Pro Lys Lys Thr Glu Ala Pro Ala Ala Pro Ala Ala Gln Glu Thr Lys  150  155  160	/16
agt gac ggg gcc cca gct tca gac tca aaa ccc ggc agc tcg gag gct Ser Asp Gly Ala Pro Ala Ser Asp Ser Lys Pro Gly Ser Ser Glu Ala 165 170 175	764
gcc ccc tct tcc aag gag acc ccc gca gcc acg gaa gcg cct agt tcc Ala Pro Ser Ser Lys Glu Thr Pro Ala Ala Thr Glu Ala Pro Ser Ser 180 185 190 195	812
aca ccc aag gcc cag ggc ccc gca gcc tct gca gaa gag ccc aag ccg Thr Pro Lys Ala Gln Gly Pro Ala Ala Ser Ala Glu Glu Pro Lys Pro 200 205 210	860
gtg gag gcc ccg gca gct aat tcc gac caa acc gta acc gtg aaa gag Val Glu Ala Pro Ala Ala Asn Ser Asp Gln Thr Val Thr Val Lys Glu 215 220 225	908
tga caag gacagcctat aggaaaaaca ataccactta aaacaatctc ctctctct *	965
ctctctctc ctctatct ctctctatct cctctctct tctcctctcc tatctctcct	1025
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attetteete teeagatatt tttgggagtg acaaacatte teteateeta ettageetae	1565
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<220>

<sup>&</sup>lt;210> 158

<sup>&</sup>lt;211> 1521

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<221> CDS <222> (417)..(1403)

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	at cag cta caa gga aag gag gaa aga sp Gln Leu Gln Gly Lys Glu Glu Arg 170 175	944
	ct gaa aag gaa tat ata gaa cat tgt hr Glu Lys Glu Tyr Ile Glu His Cys 185 190	992
Asn Thr Pro Thr Thr Asp Ser A	at tca tct ata gca gtt aaa gca cta sp Ser Ser Ile Ala Val Lys Ala Leu 00 205	1040
	tt aca tgc ttt caa caa gag tct ctt al Thr Cys Phe Gln Gln Glu Ser Leu 220	1088
	ga aaa tct cag caa cct gag tca aaa ly Lys Ser Gln Gln Pro Glu Ser Lys 235 240	1136
	aa aaa agt gct act tgt tca aat gag lu Lys Ser Ala Thr Cys Ser Asn Glu 250 255	1184
	ca gta ata act gaa gag aaa gaa aca er Val Ile Thr Glu Glu Lys Glu Thr 265 270	1232
Asp Gly Asp His Leu Ser Ser Le	ta ctg aac aaa act acg gtt cac aat eu Leu Asn Lys Thr Thr Val His Asn 80 285	1280
	aa gaa acc aat atg cag gat ggt agt ys Glu Thr Asn Met Gln Asp Gly Ser 300	1328
	tg acc aat tgt gca ttc agt ttt cag al Thr Asn Cys Ala Phe Ser Phe Gln 315 320	1376
aat tot ttg ota tat gat ttg ga Asn Ser Leu Leu Tyr Asp Leu As 325	at taa ttcta tataattttg gacttttaaa sp *	1428
tattaaggtt aaaaaatacc tgtatcta	aaa attgattctg ttaactgttg tcttaaaact	1488
aaaggtatta aagtataaaa ttaaaatt	ctg caa	1521

<220>

<sup>&</sup>lt;210> 159

<sup>&</sup>lt;211> 1377 <212> DNA

<sup>&</sup>lt;213> Homo sapiens

<221> CDS <222> (417)..(1259)

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caa Gln	ata Ile	gat Asp	agc Ser	ttt Phe 165	ggt Gly	tta Leu	gtt Val	aca Thr	tgc Cys 170	ttt Phe	caa Gln	caa Gln	gag Glu	tct Ser 175	ctt Leu	944
		tct Ser														992
		tct Ser 195														1040
		ggt Gly														1088
		gat Asp														1136
		gga Gly														1184
		gtc Val														1232
aat Asn	tct Ser	ttg Leu 275	cta Leu	tat Tyr	gat Asp	ttg Leu	gat Asp 280	taa *	ttct	a ta	ıtaat	tttg	gac	tttt	aaa	1284
tatt	aagg	rtt a	aaaa	atac	c tg	tato	taaa	att	gatt	ctg	ttaa	.ctgt	tg t	ctta	aaact	1344
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<211> 1611

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (510)..(1112)

<400> 160

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ttgactgcaa ggccagccca cgccgagggt ccaagcatcg ggatatgccg ccagcacctg 180
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cggaggcagt gaccacccac cctggagcc atg gtc cac gcc ttc ctc att cac Met Val His Ala Phe Leu Ile His 1 5	533
acc ttg agg gcc ccg aat act gag gac acg ggc ctt tgc cga gtg ctg Thr Leu Arg Ala Pro Asn Thr Glu Asp Thr Gly Leu Cys Arg Val Leu 10 15 20	581
tac tcc tgc gtc ttc ggt gct gag aag tca cct gat gac cca cgg ccg Tyr Ser Cys Val Phe Gly Ala Glu Lys Ser Pro Asp Asp Pro Arg Pro 25 30 35 40	629
cat ggt gcc gag agg gac agg ctt ctc cgg aag gaa cag att tta gct His Gly Ala Glu Arg Asp Arg Leu Leu Arg Lys Glu Gln Ile Leu Ala 45 50 55	677
gtg gcc agg cag gta gag tca atg tgt cgg ctg cag cag cag gca tct Val Ala Arg Gln Val Glu Ser Met Cys Arg Leu Gln Gln Gln Ala Ser 60 65 70	725
ggc cgg ccc ccc atg gac ctg cag ccg caa tcc tca gat gag caa gtg Gly Arg Pro Pro Met Asp Leu Gln Pro Gln Ser Ser Asp Glu Gln Val 75 80 85	773
ccg ctg cac gag gcc cca cgt ggg gct ttc cgc ctg gca gca gag aac Pro Leu His Glu Ala Pro Arg Gly Ala Phe Arg Leu Ala Ala Glu Asn 90 95 100	821
cct ttc cag gag cca cgg acg gtg gtg tgg ctg ggc gtg ctc tcg tta Pro Phe Gln Glu Pro Arg Thr Val Val Trp Leu Gly Val Leu Ser Leu 105 110 115 120	869
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ggc acg ctc cgg ctg ctg aca cgc ctc ctc ctt gac cac ctc cgg ctg Gly Thr Leu Arg Leu Leu Thr Arg Leu Leu Leu Asp His Leu Arg Leu 140 145 150	965
ctg gcg ccc agc acc agc ctt ctg ctg cgg gct gac cgc att gag ggc Leu Ala Pro Ser Thr Ser Leu Leu Leu Arg Ala Asp Arg Ile Glu Gly 155 160 165	1013
atc ctc acc cgc ttc ctg cca cat ggt cag ctg ctt ttc ctc aac gac  Ile Leu Thr Arg Phe Leu Pro His Gly Gln Leu Leu Phe Leu Asn Asp  170 180	1061
cag ttt gtc caa ggc ctg gag aag gaa ttc agt gcc gct tgg ccc cgc	1109

Gln Phe Val Gln Gly Leu Glu Lys Glu Phe Ser Ala Ala Trp Pro Arg 185 190 195 200	
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accgccgccg agtcgcgcgg aggcggaggc ttgggtgcgt tcaagattca gcttcacccg	180
taacccaccg cc atg gcc gag gaa ggc att gct gct gga ggt gta atg Met Ala Glu Glu Gly Ile Ala Ala Gly Gly Val Met 1 5 10	228
gac gtt aat act gct tta caa gag gtt ctg aag act gcc ctc atc cac Asp Val Asn Thr Ala Leu Gln Glu Val Leu Lys Thr Ala Leu Ile His 15 20 25	276
gat ggc cta gca cgt gga att cgc gaa gct gcc aaa gcc tta gac aag Asp Gly Leu Ala Arg Gly Ile Arg Glu Ala Ala Lys Ala Leu Asp Lys 30 35 40	324
cgc caa gcc cat ctt tgt gtg ctt gca tcc aac tgt gat gag cct atg Arg Gln Ala His Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro Met 45 50 55 60	372

tat gtc aag ttg gtg gag gcc ctt tgt gct gaa cac caa atc aac cta Tyr Val Lys Leu Val Glu Ala Leu Cys Ala Glu His Gln Ile Asn Leu 65 70 75	420
att aag gtt gat gac aac aag aaa cta gga gaa tgg gta ggc ctt tgt Ile Lys Val Asp Asp Asn Lys Lys Leu Gly Glu Trp Val Gly Leu Cys 80 85 90	468
aaa att gac aga gag ggg tgt att gcg gcc gct cta gag gat cca agc Lys Ile Asp Arg Glu Gly Cys Ile Ala Ala Ala Leu Glu Asp Pro Ser 95 100 105	516
tta cgt acg cgt gca tgc gac gtc ata gct ctt cta tag tgtcacctaa Leu Arg Thr Arg Ala Cys Asp Val Ile Ala Leu Leu * 110 115 120	565
att	568
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aac	e at Me	g gg et Gl	y Ly	aa gg /s G]	ga ga Ly As	at co sp Pr 5	ct aa o Ly	ag aa /s Ly	ig co	co Aı	ga gg cg GI	gc aa ly Ly	aa at 7s Me	ig to et Se	ca tca er Ser 15	-	3
tat Tyr	gca Ala	ttt Phe	ttt Phe	gtg Val 20	. Glr	a act	tgt Cys	cgg Arg	gag Glu 25	ı Glu	g cat u His	aaç Lys	g aaq Lys	g aag Lys 30	g cac s His	876	5
cca Pro	gat Asp	gct Ala	tca Ser 35	Val	aac Asn	tto Phe	tca Ser	gag Glu 40	Phe	tct Ser	aag Lys	g aag Lys	tgo Cys 45	Ser	a gag Glu	924	E
agg Arg	tgg Trp	aag Lys 50	Thr	atg Met	tct Ser	gct Ala	aaa Lys 55	Glu	aaa Lys	gga Gly	aaa Lys	ttt Phe 60	Glu	ı gat ı Asp	atg Met	972	•
gca Ala	aag Lys 65	Ala	gac Asp	aag Lys	gcc Ala	cgt Arg 70	tat Tyr	gaa Glu	aga Arg	gaa Glu	atg Met 75	Lys	acc Thr	tat Tyr	atc lle	1020	
cct Pro 80	ccc Pro	aaa Lys	GJA aaa	gag Glu	aca Thr 85	aaa Lys	aag Lys	aag Lys	ttc Phe	aag Lys 90	gat Asp	ccc Pro	aat Asn	gca Ala	ccc Pro 95	1068	
aag Lys	agg Arg	cct Pro	cct Pro	tcg Ser 100	gcc Ala	ttc Phe	ttc Phe	ctc Leu	ttc Phe 105	tgc Cys	tct Ser	gag Glu	tat Tyr	cgc Arg 110	Pro	1116	
aaa Lys	atc Ile	aaa Lys	gga Gly 115	gaa Glu	cat His	cct Pro	ggc Gly	ctg Leu 120	tcc Ser	att Ile	ggt Gly	gat Asp	gtt Val 125	gcg Ala	aag Lys	1164	
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gct Ala 160	gca Ala	tat Tyr	cga Arg	gct Ala	aaa Lys 165	gga Gly	aag Lys	cct Pro	gat Asp	gca Ala 170	gca Ala	aaa Lys	aag Lys	gga Gly	gtt Val 175	1308	
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Thr Phe Se														532
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gaa atc cg Glu Ile Ar	g aag	gtg a Val 1 125	acg Thr	ggc Gly	aag Lys	gac Asp	ccc Pro 130	ctg Leu	gaa Glu	cag Gln	ttc Phe	ggc Gly 135	ata Ile	676
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					Trp					Ala					ttc Phe	146
att Ile	tac Tyr	tgc Cys	tcc Ser 50	Asp	acc Thr	Gly	tgg Trp	gcc Ala 55	Val	ggc	aca Thr	gag Glu	gag Glu 60	tct Ser	gac Asp	194
			tgg Trp													242
			cgg Arg													290
Asp 95	Pro	Trp	aag Lys	Leu	Ser 100	Gln	Ser	Gly	Arg	Arg 105	Lys	Gln	Asp	Tyr	Gly 110	338
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Leu	Ser	Met	tgt Cys	Arg 195	Glu	Ala	Pro	Gly	Ser 200	Leu	Leu	Leu	Cys	Ser 205	Ala	626
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cac ttc ata gct tcg ggg atg gtc aat cag gag atg tta aac atg tct His Phe Ile Ala Ser Gly Met Val Asn Gln Glu Met Leu Asn Met Ser 25 30 35	150

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	aat Asn 55	Ile										Glu				246
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gct Ala	cag Gln	aag Lys	tgt Cys	cat His 90	act Thr	ctg Leu	caa Gln	agc Ser	atg Met 95	aat Asn	aat Asn	cat His	ttg Leu	gaa Glu 100	gca Ala	342
	ctg Leu															390
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	gaa Glu															534
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959

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Met Asp Pro Val Val Leu Ser Tyr Met Asp Ser Leu Leu	228

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				Lys					Ile					cag Gln		209
			Leu											aga Arg		257
		Ile												ctc Leu		305
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ttg Leu	atc Ile 535	gat Asp	act Thr	tta Leu	tca Ser	acc Thr 540	cca Pro	ctg Leu	act Thr	ggt Gly	cga Arg 545	atg Met	gcg Ala	ggg Gly	agc Ser	1745
tcc Ser 550	aaa Lys	gly ggg	ctg Leu	gcc Ala	ttc Phe 555	att Ile	ctg Leu	gga Gly	gct Ala	gaa Glu 560	ggc Gly	atc Ile	aaa Lys	gag Glu	cag Gln 565	1793
aac Asn	cag Gln	aag Lys	gag Glu	cgg Arg 570	gac Asp	gcc Ala	atc Ile	tgc Cys	atg Met 575	agc Ser	ctc Leu	gac Asp	ggg Gly	ctg Leu 580	cgg Arg	1841
aaa Lys	gcc Ala	gca Ala	cgg Arg 585	ctg Leu	agc Ser	tgc Cys	gct Ala	cta Leu 590	ggc Gly	gtt Val	gct Ala	gct Ala	aac Asn 595	tgc Cys	gcc Ala	1889
tca Ser	Ala	ctt Leu 600	gcc Ala	cag Gln	atg Met	Ala	gct Ala 605	gcc Ala	tcc Ser	tgt Cys	gtc Val	caa Gln 610	aaa Lys	aaa Lys	aaa Lys	1937
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				Gly	agc Ser											2129
					gtg Val			Leu								2177
					cct Pro											2225
					ctt Leu 715											2273
					cag Gln											2321
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					ggc Gly											2417
					ctc Leu											2465
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					cag Gln											2561
					gca Ala											2609
cga Arg	Lys	agc Ser 840	gcc Ala	ctc Leu	cac His	Leu	ttc Phe 845	cgc Arg	ctg Leu	ggg ggg	aat Asn	gcc Ala 850	atg Met	ctg Leu	agg Arg	2657
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													tac Tyr		3041
													gat Asp 995		3089
	Ala					Asp					Phe		aat Asn		3137
Thr					Cys					Ala			ctg Leu		3185
				Glu					Ala				gga Gly	Ala	3233
			Leu					Leu					cgc Arg 1		3281
		Leu					Lys					Pro	ata Ile .075		3329
	Gly					Leu					Gln		cag Gln		3377

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acc ggt ctg ata gaa gtc tgg ata atc ctg ctg gag cag ctg aca gcg Thr Gly Leu Ile Glu Val Trp Ile Ile Leu Leu Glu Gln Leu Thr Ala 1110 1115 1120 1125	3473
gct gtg tcc aat tgt cca cgg cag cac caa cca cca act ctg gat tta Ala Val Ser Asn Cys Pro Arg Gln His Gln Pro Pro Thr Leu Asp Leu 1130 1135 1140	3521
ctc ttt gag ctg ttg aga gat gtg acg aaa aca cca gga cca ggg ttt Leu Phe Glu Leu Leu Arg Asp Val Thr Lys Thr Pro Gly Pro Gly Phe 1145 1150 1155	3569
ggt atc tat gca gtg gtt cac ctc ctc ctt cct gtg atg tcc gtt tgg Gly Ile Tyr Ala Val Val His Leu Leu Pro Val Met Ser Val Trp 1160 1165 1170	3617
ctc cgc cgg agc cat aaa gac cat tcc tac tgg gat atg gcc tct gcc Leu Arg Arg Ser His Lys Asp His Ser Tyr Trp Asp Met Ala Ser Ala 1175 1180 1185	3665
aat ttc aag cac gct att ggt ctg tcc tgt gag ctg gtg gtg gag cac Asn Phe Lys His Ala Ile Gly Leu Ser Cys Glu Leu Val Val Glu His 1190 1195 1200 1205	3713
att caa agc ttt cta cat tca gat atc agg tac gag agc atg atc aat Ile Gln Ser Phe Leu His Ser Asp Ile Arg Tyr Glu Ser Met Ile Asn 1210 1215 1220	3761
acc atg ctg aag gac ctc ttt gag ttg ctg gtc gcc tgt gtg gcc aag Thr Met Leu Lys Asp Leu Phe Glu Leu Leu Val Ala Cys Val Ala Lys 1225 1230 1235	3809
ccc act gaa acc atc tcc aga gtg ggc tgc tcc tgt att aga tac gtc Pro Thr Glu Thr Ile Ser Arg Val Gly Cys Ser Cys Ile Arg Tyr Val 1240 1245 1250	3857
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	Glu	tac Tyr 1320				Arg					Gln					4097
Asp		cag Gln	_		Pro	_				Asn		_		_	_	4145
		cag Gln		Ile			_		Pro	-	-			Asn		4193
		aag Lys	Lys					Arg					Ser			4241
		cag Gln	-			_	Asn			-		Leu		-		4289
	Val	aaa Lys 1400				Pro			-	_	Thr					4337
Glu		aag Lys			Gly					Ile		_	_		_	4385
		ata Ile		Asp					Ser					Arg		4433
		acc Thr	Ser					Cys					Val			4481
		ggc Gly 1					Tyr					Met				4529
	Tyr	ttc Phe 1480				Val					Thr					4577
Ile		gcc Ala			Val					Phe						4625
		gat Asp		Ser					Ser					Ile		4673
		acc Thr	Ala					Pro					Lys			4721
tgg	cgg	gca	cgg	atg	ccc	ttg	ctc	agc	gtc	cag	cct	gtc	agc	aac	gca	4769

Trp Arg Ala Arg Met Pro Leu Leu Ser Val Gln Pro Val Ser Asn Ala 1545 1550 1555	
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tgc aac aac tac atc cag atg cac ttg gac ctg gag aac tgt atg gag Cys Asn Asn Tyr Ile Gln Met His Leu Asp Leu Glu Asn Cys Met Glu 1575 1580 1585	4865
gag cct ccc atc ttc aag ggc gac ccg ttc ttc atc ctg ccc tcc ttc Glu Pro Pro Ile Phe Lys Gly Asp Pro Phe Phe Ile Leu Pro Ser Phe 1590 1595 1600 1605	4913
cag tee gag tea tee ace eea tee ace ggg gge tte tet ggg aaa gaa Gln Ser Glu Ser Ser Thr Pro Ser Thr Gly Gly Phe Ser Gly Lys Glu 1610 1615 1620	4961
acc cct tcc gag gat gac aga agc cag tcc cgg gag cac atg ggc gag Thr Pro Ser Glu Asp Asp Arg Ser Gln Ser Arg Glu His Met Gly Glu 1625 1630 1635	5009
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ccc aaa gtg gag aag aag gat ccc agc cgg aag aag gag tgg tgg gag Pro Lys Val Glu Lys Lys Asp Pro Ser Arg Lys Lys Glu Trp Trp Glu 1655 1660 1665	5105
aat gcg ggg aac aaa atc tac acc atg gca gcc gac aag acc att tca Asn Ala Gly Asn Lys Ile Tyr Thr Met Ala Ala Asp Lys Thr Ile Ser 1670 1675 1680 1685	5153
aag ttg atg acc gaa tac aaa aag agg aaa cag cag cac aac ctg tcc Lys Leu Met Thr Glu Tyr Lys Lys Arg Lys Gln Gln His Asn Leu Ser 1690 1695 1700	5201
gcg ttc ccc aaa gag gtc aaa gtg gag aag aaa gga gag cca ctg ggt Ala Phe Pro Lys Glu Val Lys Val Glu Lys Lys Gly Glu Pro Leu Gly 1705 1710 1715	5249
ccc agg ggc cag gac tcc ccg ctg ctt cag cgt ccc cag cac ttg atg Pro Arg Gly Gln Asp Ser Pro Leu Leu Gln Arg Pro Gln His Leu Met 1720 1725 1730	5297
gac caa ggg caa atg cgg cat tcc ttc agc gca ggc ccc gag ctg ctg Asp Gln Gly Gln Met Arg His Ser Phe Ser Ala Gly Pro Glu Leu Leu 1735 1740 1745	5345
cga cag gac aag agg ccc cgc tca ggc tcc acc ggg agc tcc ctc agt Arg Gln Asp Lys Arg Pro Arg Ser Gly Ser Thr Gly Ser Ser Leu Ser 1750 1765	5393
gtc tcg gtg aga gac gca gaa gca cag atc cag gca tgg acc aac atg Val Ser Val Arg Asp Ala Glu Ala Gln Ile Gln Ala Trp Thr Asn Met	5441

gtg cta aca gtt ctc aat cag att cag att ctc cca gac cag acc ttc
Val Leu Thr Val Leu Asn Gln Ile Gln Ile Leu Pro Asp Gln Thr Phe
1785

acg gcc ctc cag ccc gca gtg ttc ccg tgc atc agt cag ctg acc tgt
Thr Ala Leu Gln Pro Ala Val Phe Pro Cys Ile Ser Gln Leu Thr Cys
1800

1805

1780

5489

5489

5537

cac gtg acc gac atc aga gtt cgc cag gct gtg agg gag tgg ctg ggc
His Val Thr Asp Ile Arg Val Arg Gln Ala Val Arg Glu Trp Leu Gly
1815
1820
1825

agg gtg ggc cgt gtc tat gac atc att gtg tag ccgactcc tgttctactc 5636 Arg Val Gly Arg Val Tyr Asp Ile Ile Val \* 1830 1835 1840

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5696

6656

6716

6776

6836

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<213> Homo sapiens

<220>

<221> CDS

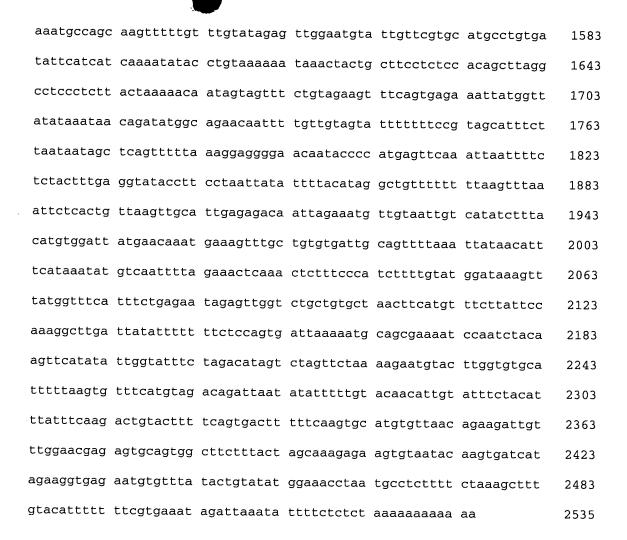
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<400> 169

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aatagtatta aaagtcagag gctttactaa tctacctata tgtattccat ggctaacaaa 240
ccctggcccc tttacat atg agc tct gga ggt tcg cct ggc tgc ctc agg
Met Ser Ser Gly Gly Ser Pro Gly Cys Leu Arg
1 5 10

ctt gca gaa ggc tgc ccc aat cac aga gcc tgg gta agg tgg aac agg Leu Ala Glu Gly Cys Pro Asn His Arg Ala Trp Val Arg Trp Asn Arg 15 20 25 338

agg Arg	cag Gln	ccc Pro 30	cac His	tcg Ser	gct Ala	ttt Phe	ctg Leu 35	att Ile	gca Ala	tcc Ser	cac His	ctg Leu 40	ttt Phe	ctg Leu	agt Ser	386
gtg Val	ttg Leu 45	gtt Val	tgg Trp	ttt Phe	aat Asn	tct Ser 50	ttt Phe	caa Gln	ggg Gly	ttg Leu	gag Glu 55	ttg Leu	gaa Glu	agt Ser	gaa Glu	434
aac Asn 60	cct Pro	aga Arg	cac His	ttg Leu	ctg Leu 65	tgg Trp	aat Asn	gtt Val	tgc Cys	ctg Leu 70	gtt Val	gta Val	ttg Leu	gtg Val	tgt Cys 75	482
			tca Ser													530
tgt Cys	tct Ser	gtt Val	gaa Glu 95	agc Ser	cac His	agg Arg	acc Thr	aaa Lys 100	agg Arg	aaa Lys	ata Ile	ttg Leu	caa Gln 105	cta Leu	ttt Phe	578
gca Ala	Asn	ata Ile 110	ctt Leu	ccc Pro	tac Tyr	cta Leu	tac Tyr 115	aag Lys	cag Gln	cca Pro	tat Tyr	act Thr 120	aaa Lys	aag Lys	cac His	626
taa *	acaa	gca	ıcaaa	ıtga	acac	taaa	ta g	cctt	atac	c aa	ıaaag	catt	ctt	gtaa	ctg	683
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gccct	acaa	ac t	atct	tctgt	tt!	taga	aatt	tgta	agtca	act (	gttc	tag	tg c	cact	ggaaa	1463
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<211> 2191

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<213> Homo sapiens

<220>

<221> CDS

<222> (451)..(846)

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aaagctgata ataatattga tgctaatgaa gaaactctag aaacagatta tacaactatt	360
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aat gtt att gaa gat aac aaa agt gag aat atc tta gaa aat aca gac Asn Val Ile Glu Asp Asn Lys Ser Glu Asn Ile Leu Glu Asn Thr Asp 25 30 35	567
tct atg gag aca gat gaa atc att cct att ttg gaa aag ctt gca cct Ser Met Glu Thr Asp Glu Ile Ile Pro Ile Leu Glu Lys Leu Ala Pro 40 45 50 55	615
tct gag gat gaa ctt act tgc ttt tct aaa aca tct ctc ctt cca atc Ser Glu Asp Glu Leu Thr Cys Phe Ser Lys Thr Ser Leu Leu Pro Ile 60 65 70	663
gat gag aca aat cca gat ttg gaa gag aaa atg gaa agt tct ttt ggt Asp Glu Thr Asn Pro Asp Leu Glu Glu Lys Met Glu Ser Ser Phe Gly 75 80 85	711
tca cca tct aaa caa gaa agt agt gag agt ttg cca aaa gaa gcc ttt Ser Pro Ser Lys Gln Glu Ser Ser Glu Ser Leu Pro Lys Glu Ala Phe 90 95 100	759
ctg gtc ctc tct gat gaa gag gat att tcg ggt gaa aaa gat gag tct Leu Val Leu Ser Asp Glu Glu Asp Ile Ser Gly Glu Lys Asp Glu Ser 105 110 115	807
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<211> 874

<212> DNA

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<400> 171

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ttgcacgtat tcgtcatagg atg ctg tgg ccc ggc gca gga ttg gag gga 170

Met Leu Trp Pro Gly Ala Gly Leu Glu Gly

1 5 10

cat aga cct ggt gga agg cgt ggc gcc ctg acc cag gga ttt ggc
His Arg Pro Gly Gly Arg Arg Gly Ala Ala Leu Thr Gln Gly Phe Gly
15 20 25

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cto Lei	g acc ı Thr	ccc Pro	gtg Val 80	. Arg	r cct	gac Asp	ago Arg	acc Thr 85	Pro	cgc Arg	cca Pro	a gco o Ala	agc Ser 90	Pro	gga Gly	290
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gco Ala	gtc Val 110	Pro	gcc Ala	agc Ser	ctc Leu	gac Asp 115	gtt Val	tgt Cys	gac Asp	aac Asn	tgg Trp 120	Leu	cgg Arg	ccg Pro	gag Glu	386
ccc Pro 125	Pro	ggc	cag Gln	gaa Glu	gcc Ala 130	cga Arg	gtg Val	cag Gln	agc Ser	tgg Trp 135	aag Lys	gag Glu	gag Glu	gag Glu	aag Lys 140	434
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ggc agc atc cag atg aac cac aac tcc ttc ctc agc gca acc agg cca Gly Ser Ile Gln Met Asn His Asn Ser Phe Leu Ser Ala Thr Arg Pro 15 20 25	217
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	gtt ctt tct Val Leu Ser 65						361
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	ggg atc tct Gly Ile Ser						457
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85						90		95				
_		-		_		_	_			•	ctt Leu	

391

aaa Lys

	ctg Leu				_	_		_	-	_	_	_	439
115	cac	ata	++-	~~~	120	225	 	0 = 0	125	 		 130	487

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Lys Asn Lys Gln Lys Ile Asp Leu Asp Ser Met Glu Asn Ser Glu Arg
180 185 190

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Val Ile Gln His Val Phe Gln Asn Leu Ile Leu Gly Ser Lys Val Asn
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220
225

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								cgt Arg 70								242
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								atc Ile								434
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gca	aac	gcc	ttc	aac	aac	agc	att	att	cca	gaa	gac	acc	ttc	ttc	ccc	674

Ala	Asn	Ala	Phe	Asn 210	Asn	Ser	Ile	Ile	Pro 215	Glu	Asp	Thr	Phe	Phe 220	Pro	
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	gat Asp															770
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_	tgg Trp		_	tga *	g											834
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	gat Asp															246

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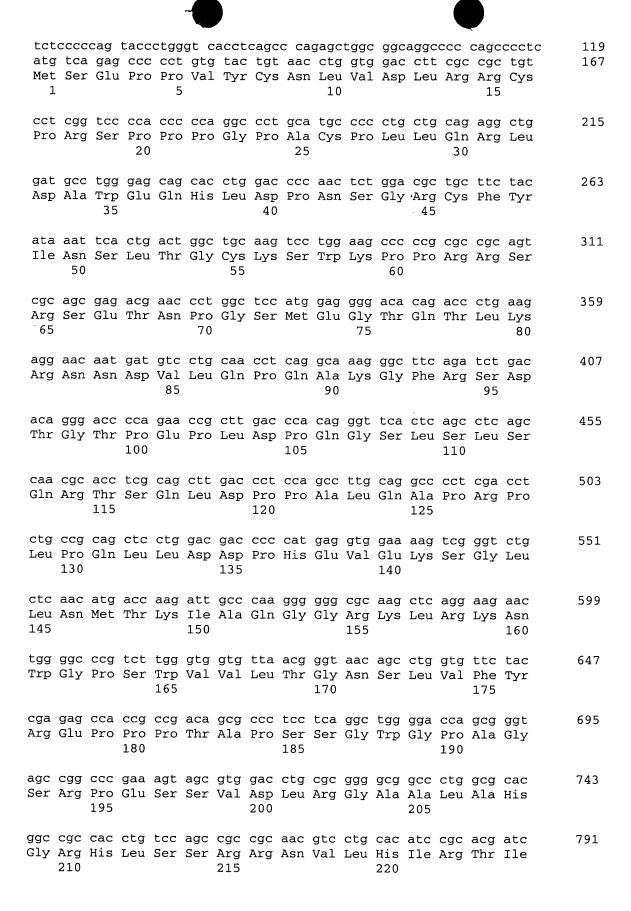
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	_	-		~					_					caa Gln		466
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gaaa	gctg	gtg g	gtttc	ctctt	t aa	caga	ttca	ggg	gaato	atc	cttt	gact	cg g	gacca	agaag	698
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gcc tgg cac cgc gcg ctg cgg act gtc atc gag cgg ctg gat cgg gag Ala Trp His Arg Ala Leu Arg Thr Val Ile Glu Arg Leu Asp Arg Glu 245 250 255	887
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														ctg Leu 30		214
	_	_	_										_	gtg Val		262
	_	_		_					-					gtc Val		310
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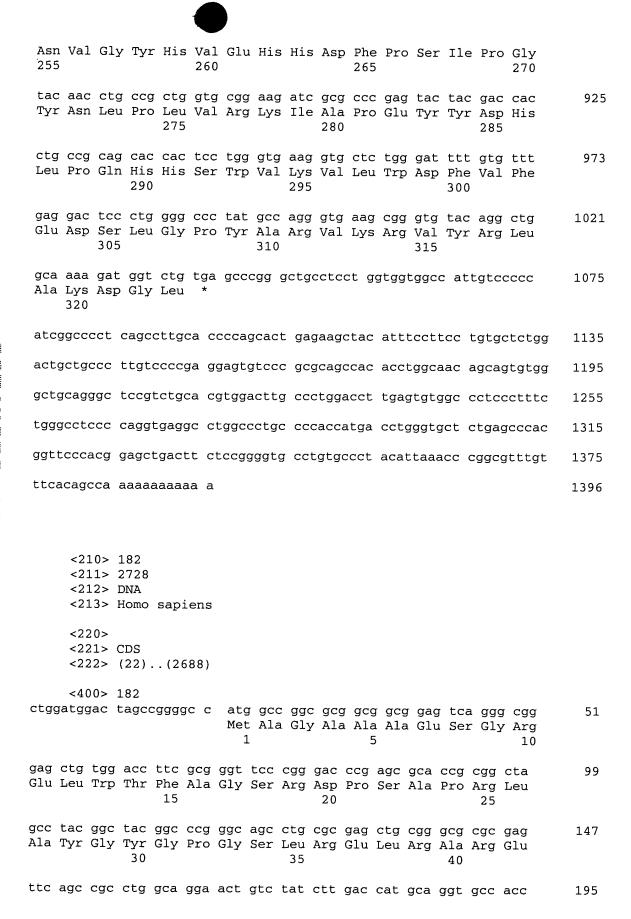
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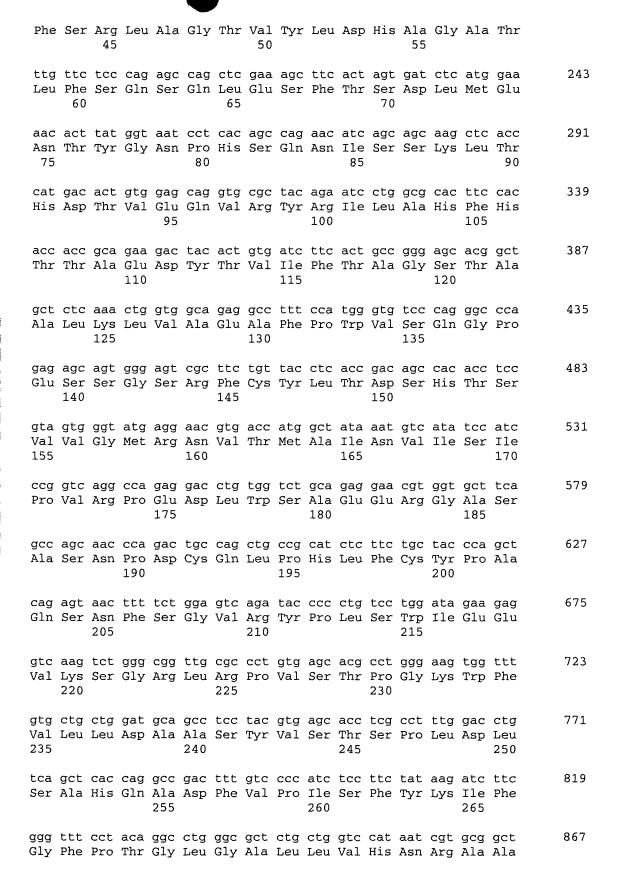
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gcc cat ctt tgt gtg ctg tgt gtg ctt gca tcc aac tgt gat gag cct Ala His Leu Cys Val Leu Cys Val Leu Ala Ser Asn Cys Asp Glu Pro 50 55 60	374
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							cag Gln									253
							ctg Leu 70									301
							ctg Leu									349
							gcg Ala									397
							gtg Val									445
							tac Tyr									493
							ggc Gly 150									541
							cag Gln									589
							gtg Val									637
							ctg Leu									685
							gcc Ala									733
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aat	gtg	ggc	tac	cac	gtg	gag	cac	cac	gac	ttc	ccc	agc	atc	ccg	ggc	877





270 275 280

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gga Gly	ttt Phe	gac Asp	acc Thr	cta Leu 335	gag Glu	cgc Arg	ctc Leu	aca Thr	ggt Gly 340	gga Gly	atg Met	gag Glu	aat Asn	ata Ile 345	aag Lys	1059
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Gly ggg	cag Gln 460	ccc Pro	aca Thr	gga Gly	tct Ser	gtg Val 465	agg Arg	att Ile	tca Ser	ttt Phe	gga Gly 470	tac Tyr	atg Met	tcg Ser	acg Thr	1443
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		_	-	gtc Val 560	-	_	_	_				~ ~		1731
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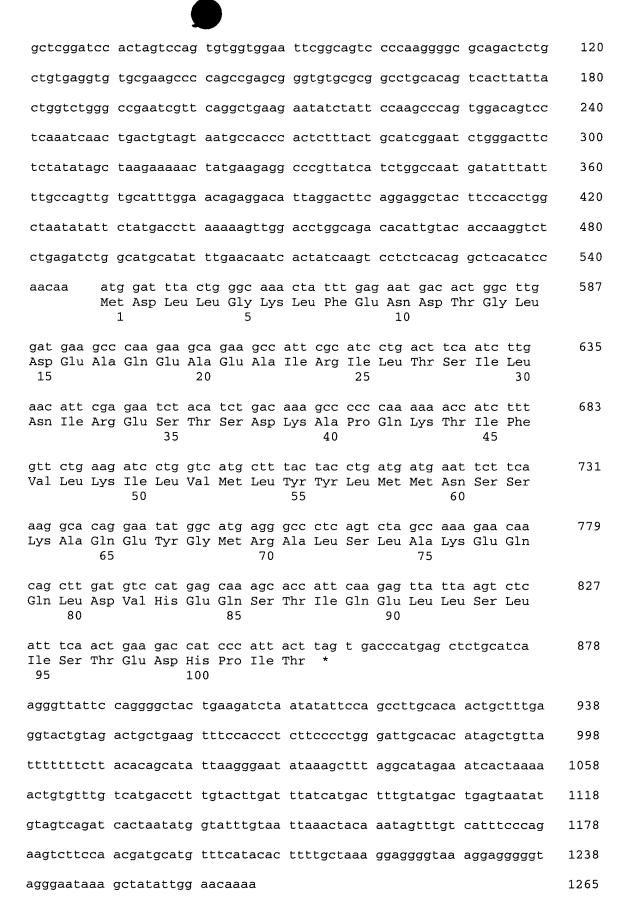
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Harli Harri	tgc tg Cys Cy 1	rc agt rs Ser .5	aac Asn	gtg Val	atc Ile	ttc Phe 20	Leu	gag Glu	ctc Leu	ctg Leu	gcc Ala 25	cgg Arg	aag Lys	cat His	cca Pro	337
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tonk theel thin	gaa gg Glu Gl	c ttc y Phe	ctc Leu	ttt Phe 50	gaa Glu	gct Ala	gat Asp	ttg Leu	gga Gly 55	agg Arg	aag Lys	cca Pro	cca Pro	gct Ala 60	atc Ile	433
	cca at Pro Il			Tyr												481
	gtg gt Val Va	-	Asn		_											529
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	atc at Ile Il 110	t ttg e Leu	aag Lys	aaa Lys	aga Arg 115	tac Tyr	agt Ser	ata Ile	ttc Phe	aaa Lys 120	tat Tyr	acc Thr	tcc Ser	att Ile	gcc Ala 125	625
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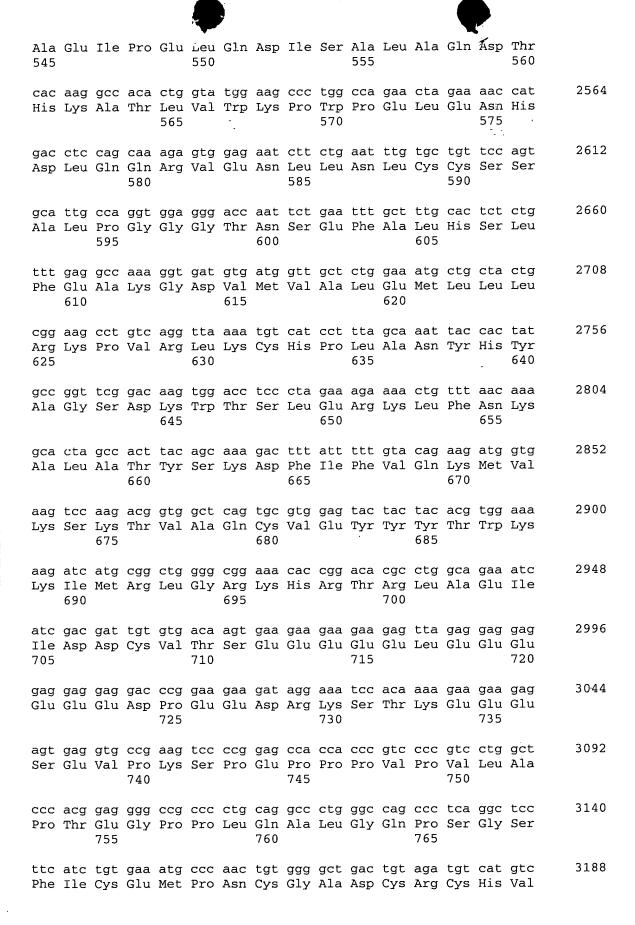
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90

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	_	_	_	-	cag Gln 150		_	_	_			_			_	1316
			_		tat Tyr	-				-	_	-		_		1364
	_	-	_		cag Gln	-		_	_							1412
			-		acc Thr			_	_			-	-	_		1460
	_			-	tcc Ser	-				_				_		1508
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gca	gaa	atc	cct	gaa	ctc	caa	gat	atc	tct	gcc	ctg	gcc	cag	gac	aca	2516



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		-	_	-	gtc Val	_		_	_			_	_			3668
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Thr Lys Pro Met Ala Gln Arg Ser Ala His Cys Ser Arg Pro Ser Gly

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			_		tat Tyr								_	600
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					aac Asn									792
		_			att Ile		_		_	_	-			840
					aaa Lys									888
			_	_	tat Tyr 180	_			-					936
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gtt cac gta gat tct ggt gca tct gca ata act cga gaa agc cac aca Val His Val Asp Ser Gly Ala Ser Ala Ile Thr Arg Glu Ser His Thr 305 310 315	1320
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gct aag tgc tgc tgt ttc ttt aag agg aaa agg aag aag act gct cag Ala Lys Cys Cys Phe Phe Lys Arg Lys Arg Lys Thr Ala Gln 370 375 380	1512
cgc cac aag tga cca gtgcctccca ggagtcctca ggccctgggg actctgactc Arg His Lys * 385	1567
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	75					80					85					
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							gtt Val									1059
							cac His									1107
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ggc atc tct ggg a Gly Ile Ser Gly I				
agg tac ctg gac c Arg Tyr Leu Asp I 50	-			_
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tat ggg aaa ttc c Tyr Gly Lys Phe A				
ctg gag ttt ctt c Leu Glu Phe Leu I 95				
tac agt ttc act o Tyr Ser Phe Thr I 1				
gaa tca gtg gct a Glu Ser Val Ala I 130	Ile Leu Pro Gln L	_		
gag gct gag acc a Glu Ala Glu Thr I 145				
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ttc tat gac caa a Phe Tyr Asp Gln I 175				
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ggcggggcg cacgactgac tggctggacc atg aac gtg ttc cga atc ctc
Met Asn Val Phe Arg Ile Leu
1 5
ggc gac ctg agc cac ctc ctg gcc atg atc ttg ctg ggg aag atc 219

tgg agg tcc aag tgc tgc aag ggc atc tct ggg aag agc cag atc ctg
Trp Arg Ser Lys Cys Lys Gly Ile Ser Gly Lys Ser Gln Ile Leu
25 30 35

Gly Asp Leu Ser His Leu Leu Ala Met Ile Leu Leu Gly Lys Ile

15

			gtc Val								ctg Leu					31!
											tgg Trp					363
											ttc Phe					411
			_								ctg Leu			_		459
											aag Lys 115			_		507
											gga Gly					555
											acc Thr					603
			tta Leu 155							tga *	ggac	ctto	aga	ıgaca	igtc	654
tacg	cctt	aa c	caago	acat	g aa	ıggaa	acta	ttt	tgaa	tgt	tctc	tttg	gc a	actt	atcca	714
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tgt ttt atg gtc acc tac cca ctt aca cct gac cct ggg gcc tct gca Cys Phe Met Val Thr Tyr Pro Leu Thr Pro Asp Pro Gly Ala Ser Ala 15 20 25	460								
gtt ttc ttg gcg ttg tca cca caa aag gaa gaa gcc cac ctg tgg ctg Val Phe Leu Ala Leu Ser Pro Gln Lys Glu Glu Ala His Leu Trp Leu 30 35 40	508								
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tgg ctt ctt gaa ggc aga cac aag tct gca ggc tgc tca cgt cat ctc Trp Leu Leu Glu Gly Arg His Lys Ser Ala Gly Cys Ser Arg His Leu 60 65 70 75	604								
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ggc ctt ggc cct gcc ctg tcc ctg cca tgc aac ttc aca act cag ctg Gly Leu Gly Pro Ala Leu Ser Leu Pro Cys Asn Phe Thr Thr Gln Leu 95 100 105	700								
gcc tag acccctggga ggcctccaag tccctaaggt tagacatctc ctggggtgct 7 Ala *									
atggactgtc ggggctccaa ggagccgagt gtgggggaaa ctcactgtgg gaggcgctcc	816								
tgacctgcag ggagctggaa tgctgtggga gggccctgac cccggggccc atggagctcc	876								
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<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

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gta cag gtg ct Val Gln Val Le 20						151
cag gct ccg aa Gln Ala Pro As						199
agc caa atg tc Ser Gln Met Se 5	r Leu Pro A					247
gtg gag cag cc Val Glu Gln Pr 70	a att ata a o Ile Ile T	cc caa gga nr Gln Gly 75	tcc tct Ser Ser	gtt aca a Val Thr I 80	ag ata act ys Ile Thr	295
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tct gtg cct aa Ser Val Pro Ly 100						391
gcc tct gag aa Ala Ser Glu Ly						439
gaa gct cag at Glu Ala Gln I1 13		sn Val Glu	His Met	Ile Val A		487
aag aag gct ct Lys Lys Ala Le 150						535
ccc tcc acc ca Pro Ser Thr Hi 165	s Met Val V					583
caa cag aaa tg Gln Gln Lys Cy 180						631
tcc cta acg ac Ser Leu Thr Th						679

cag ttc atg cgt att cag aat gta ggc caa aag aaa gct gaa gag agt Gln Phe Met Arg Ile Gln Asn Val Gly Gln Lys Lys Ala Glu Glu Ser 215 220 225	727
cca gca gaa att atc atc cag gct att cct cag tat gct att cct tgt Pro Ala Glu Ile Ile Ile Gln Ala Ile Pro Gln Tyr Ala Ile Pro Cys 230 235 240	775
cac tcc agc tcc aat gtg gtg gtg gag ccc agt ggg ctt ctt gag cta His Ser Ser Ser Asn Val Val Glu Pro Ser Gly Leu Leu Glu Leu 245 250 255	823
aac aac ttc act agt caa cag ctg gat gat gag gag aca gca atg gag Asn Asn Phe Thr Ser Gln Gln Leu Asp Asp Glu Glu Thr Ala Met Glu 260 275	871
cag gac ata gac agt agc acg gag gat gga act gaa ccc agc cct tct Gln Asp Ile Asp Ser Ser Thr Glu Asp Gly Thr Glu Pro Ser Pro Ser 280 285 290	919
cag agc tct gct gaa cgg tcc tag tgtttggaca caatagtgca ctttaaaacc Gln Ser Ser Ala Glu Arg Ser * 295	973
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gcccgtactt aggctgtgga ccctaaaaca gcagtgtttc aacaagatgt tgctgcagga	1093
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ctc aaa gag gct gaa gaa gag cga cta aaa gct gca cag tat ggt tta Leu Lys Glu Ala Glu Glu Glu Arg Leu Lys Ala Ala Gln Tyr Gly Leu 15 20 25	278

		_		_		aat Asn 35	-		_			_	-		_	326
						atg Met										374
			_	_	_	gaa Glu		_	_	_	-		_	_	-	422
_	_	-	_	_	_	att Ile						_		_		470
	_	_	_			agc Ser	_	-			_	-			_	518
						aaa Lys 115										566
	-	_	_	-	_	aag Lys			_	-		-	_	_		614
						gaa Glu										662
-	_	_				atg Met	_	_					_		_	710
_		_	_	_		acc Thr			_	-			_			758
	_		_	_		gaa Glu 195							_	_	-	806
-	_					gaa Glu		_		_			_	_	_	854
				_		gag Glu		_	_	-	-			_		902
_	_	_	_	-	-	gca Ala		_		-	_	_			_	950
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														aaa Lys		1190
														tat Tyr		1238
														gat Asp		1286
														aac Asn		1334
														aaa Lys 395		1382
														ttt Phe		1430
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gac aga gga aaa att ggc aag gtt Asp Arg Gly Lys Ile Gly Lys Val 40	gaa ggt cac Glu Gly His 45	cag cac att cag gtt Gln His Ile Gln Val 50	680
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_		_				ttc Phe			_			_	_			241
		_			-	cgg Arg		_	_	-	_	-				289
_	~ ~				_	acc Thr		_		_			_			337
						ggt Gly			_		-		_		_	385
						gtg Val 130								-		433
						gat Asp			_	_	-	-			-	481
	_		_	_	_	att Ile		_				_		_		529
						cga Arg										577
						atc Ile										625
	_		-	-	_	ctt Leu 210	_							_		673
						ctc Leu										721
aag	aag	cca	aga	tgc	taa	gcta	ag g	rtgac	tata	g ca	ccct	.ggct	gtt	ttct	tct	775

Lys Lys Pro Arg Cys * 240	
ggggcttagt cgaatcagct ttgtaatgtt atgggacaaa aatcaattat ctcattaatg	835
ttttagtctg ctgcacacat ctaaaaaagc aaaatggcaa taaaatcata acagtgaaaa	895
aaaaaaaa	903
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att cta gct aac cgc gtc ggg gag cgg cgc cgg gag aag ggc gag gcg Ile Leu Ala Asn Arg Val Gly Glu Arg Arg Arg Glu Lys Gly Glu Ala 30 35 40	147
act tgc atc acg gag atg tcg gtg atg atg gct tgc tgg aag cag aat Thr Cys Ile Thr Glu Met Ser Val Met Met Ala Cys Trp Lys Gln Asn 45 50 55	195
gaa ttc cgc gac gat gcg tgc aga aaa gag atc cag ggc ttc ctc gat Glu Phe Arg Asp Asp Ala Cys Arg Lys Glu Ile Gln Gly Phe Leu Asp 60 65 70 75	243
tgt gcc gcg agg gct cag gtg acc gat ggc tcc tgg ggt gct ttc tca Cys Ala Ala Arg Ala Gln Val Thr Asp Gly Ser Trp Gly Ala Phe Ser 80 85 90	291
gga aaa gaa tgg ggg aga tag aa gtaatgattc tccctgcctt ttgctaggaa Gly Lys Glu Trp Gly Arg * . 95	344
aggccctttc attcatttgg gaggtatatt attcacgcca aagtgggaaa ggttacagtt	404

464

524

584

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ttgaaggctg tgtgatcttg acggatttat tcattgctct gaactttcga gttactgtac

gtaaaatgag gctaaccaat accaccttaa agaatgttgt gagtgtcaga tgaagtaatg

aatgggaaaa tcattttgaa aaatgtaaat tgctgctcaa gtagacatta ttgtgtgaaa

tagaactaaa gagactaaac taaataatga caatagtttg gttcctgtct aggctaattg	644
ctagg	649
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ttc gtg atg ggt tgc gcc gtg ggc atg gcg gcc gag gcg ctc ttc ggc Phe Val Met Gly Cys Ala Val Gly Met Ala Ala Glu Ala Leu Phe Gly 25 30 35	149
acc ttt tcc tgt ctc agg atc gga atg cgg ggt cga gag ctg atg ggc Thr Phe Ser Cys Leu Arg Ile Gly Met Arg Gly Arg Glu Leu Met Gly 40 45 50	197
ggc att ggg aaa acc atg atg cag agt ggc ggc acc ttt ggc aca ttc Gly Ile Gly Lys Thr Met Met Gln Ser Gly Gly Thr Phe Gly Thr Phe 55 60 65 70	245
atg gcc att ggg atg ggc atc cga tgc taa c catggttgcc aactacatct Met Ala Ile Gly Met Gly Ile Arg Cys * 75 80	296
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aaaa	360

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<sup>&</sup>lt;220>

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ggccatcttt ctggggagga ctctcccagg tagggaaggc cagaggtggc ccagtgcctg	180
gagggttagg gtctctgcct gggat atg caa gag gaa gta gga aag gga ggt Met Gln Glu Glu Val Gly Lys Gly Gly 1 5	232
ctc atg gat gat cct agg ctg cta gaa gtc ctt aag gcc cca tct agt Leu Met Asp Asp Pro Arg Leu Leu Glu Val Leu Lys Ala Pro Ser Ser 10 15 20 25	280
cca ttc cac tcc cta ccc cca ttc cag agc cga gta gta agt tta cag Pro Phe His Ser Leu Pro Pro Phe Gln Ser Arg Val Val Ser Leu Gln 30 35 40	328
atg ttt ccc cca tta cgt acc ccc acc cat ccc tgc tgc agc gag cct Met Phe Pro Pro Leu Arg Thr Pro Thr His Pro Cys Cys Ser Glu Pro 45 50 55	376
gag agc cag gca gag cca ggc aca gct cct cag tct tct cac aca gtc Glu Ser Gln Ala Glu Pro Gly Thr Ala Pro Gln Ser Ser His Thr Val	424
ctg ccg gtg gcc ttc cct cat gac cct tgc ttg gga ggg tgg agc act Leu Pro Val Ala Phe Pro His Asp Pro Cys Leu Gly Gly Trp Ser Thr 75 80 85	472
ggc tcc ttg acc cta aaa ggt agc tgg cag ggg caa gat ggg ggc cag Gly Ser Leu Thr Leu Lys Gly Ser Trp Gln Gly Gln Asp Gly Gly Gln 90 95 100 105	520
cta cct aat gga tga aagccacaag tgaatacagt tcttgtcacc agggttgccc Leu Pro Asn Gly * 110	575
tgccctcact cggcagggag ttctgacacc ccagggcccg tgagctacct gcttgagccc	635
ctgtttctgg ggcaccttcg aggaggcgtt gtggagggca tcgccccctg tttattcaca	695
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cccgacagca gtggggtcca cacactgagc tccagctggc actgcccact caagggctga	815
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agtgtgaata cctctgcaca tatgggtgta tctgtgtgtg ctcgtgtata tggggtgggg	1055
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1175 cgccctggcg agtgcctacc ctggcagaac ccagggagga gtggaggctg cctctgcctg 1235 ggcctccaca cagcatcctg tacatacgcc acctgggctg ggggtgggga ggcagggcca 1280 ggagcatcga ttaaagatca catcctgggg cttccaggga gctca

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gcc ttg gtg gaa gcc att gtg gaa gaa gtg gcc tgt ccc atc tgt atg Ala Leu Val Glu Ala Ile Val Glu Glu Val Ala Cys Pro Ile Cys Met 15 10 391 acc ttc ctg agg gag ccc atg agc att gac tgt ggc cac agc ttc tgc Thr Phe Leu Arg Glu Pro Met Ser Ile Asp Cys Gly His Ser Phe Cys 30 25 cac age tgt etc tet gga etc tgg gag atc eca gga gaa tee cag aac 439 His Ser Cys Leu Ser Gly Leu Trp Glu Ile Pro Gly Glu Ser Gln Asn 40 45 tgg ggt tac acc tgt ccc ctc tgt cga gct cct gtc cag cca agg aac 487 Trp Gly Tyr Thr Cys Pro Leu Cys Arg Ala Pro Val Gln Pro Arg Asn

343

55 ctg cgg cct aat tgg cag ctg gcc aat gtt gta gaa aaa gtc cgt ctg 535 Leu Arg Pro Asn Trp Gln Leu Ala Asn Val Val Glu Lys Val Arg Leu 75 80 70

cta agg cta cat cca gga atg ggg ctg aag ggt gac ctg tgt gag cgc 583 Leu Arg Leu His Pro Gly Met Gly Leu Lys Gly Asp Leu Cys Glu Arg 95 90 85

631 cat ggg gaa aag ctg aag atg ttc tgc aaa gag gat gtc ttg ata atg

His	Gly	Glu	Lys	Leu 105	Lys	Met	Phe	Cys	Lys 110	Glu	Asp	Val	Leu	Ile 115	Met	
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						tgg Trp										727
	_		_	_		gag Glu 155		-		_						775
	-					gcc Ala										823
						gag Glu										871
	_	_				cgg Arg	_	_		-						919
						gag Glu										967
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						agg Arg										1063
-	-		-	-		tta Leu										1111
_		-				ctg Leu		_	_		_	-	_		-	1159
						aag Lys										1207
	-		_			cgt Arg 315			-				-			1255
						aac Asn										1303

325	330	335	340
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ccc cac tat gga ttc Pro His Tyr Gly Phe 390			
cga gca ggc acc gat Arg Ala Gly Thr Asp 405			
cgc cgg gtg gga atc Arg Arg Val Gly Ile 425			
tac aat gtg act gac Tyr Asn Val Thr Asp 440	Cys Gly Ser Hi		_
ccc ttc cct ggg cgc Pro Phe Pro Gly Arg 455	-		_
gga acc aac aac act Gly Thr Asn Asn Thr 470		-	
gac taa gaaagctacc a Asp * 485	accctaacca caga	aggettg gaattgggee	tggccccat 1791
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60

120

180

240

300

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Met Arg Leu Phe Val Ser Val

act gtc ctt gtc atc tgt ctt gca gat tta gaa gag gaa tca gaa agc 399
Thr Val Leu Val Ile Cys Leu Ala Asp Leu Glu Glu Glu Ser Glu Ser
10 15 20

tgg gac aac tct gag gct gaa gag gag gag aaa gcc cct gtg ttg cca 447
Trp Asp Asn Ser Glu Ala Glu Glu Glu Glu Lys Ala Pro Val Leu Pro
25 30 35

gag agt aca gaa ggg cgg gag ctg acc cag ggc ccg gca gag tcc tcc

Glu Ser Thr Glu Gly Arg Glu Leu Thr Gln Gly Pro Ala Glu Ser Ser

40

45

50

55

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Ser Leu Ser Gly Cys Gly Ser Trp Gln Pro Arg Lys Leu Pro Val Phe

60

65

70

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Lys Ser Leu Arg His Met Arg Gln Val Leu Gly Ala Pro Ser Phe Arg
75 80 85

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ctt ccc gtg ggc Leu Pro Val Gly 120	tgc gtc cg Cys Val Ar 125	c atc atc co g Ile Ile Pı	ca tac agc ro Tyr Ser 130	agc cag tac Ser Gln Tyr	gag 735 Glu 135
gag gcc tat cgg Glu Ala Tyr Arg	tgc aac tt Cys Asn Ph 140	e Leu Gly Le	tc agc ccg eu Ser Pro 45	cac gtg cag His Val Gln 150	Ile
ccc ccc cac gtg Pro Pro His Val 155	Leu Ser Se				
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tct ctc agc aag Ser Leu Ser Lys 185	tac gag tt Tyr Glu Ph 19	e Val Val Th	cc agt ggg hr Ser Gly 195	agc cct gta Ser Pro Val	gct 927 Ala
gca gac cga gtg Ala Asp Arg Val 200	ggc ccc ac Gly Pro Th 205	c atc ctg aa r Ile Leu As	at aag att sn Lys Ile 210	gaa gcg gct Glu Ala Ala	ctg 975 Leu 215
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								ato	g cto	g aca	a cac	c cco	c ctt	caç	r GJA a aaa	113
cct Pro	ggc Gly 10	ctt Leu	gac Asp	tta Leu	gly ggg	ctg Leu 15	cac His	tgt Cys	atc Ile	ctc Leu	agc Ser 20	aac Asn	ggc Gly	ctt Leu	gca Ala	161
gga Gly 25	gcc Ala	cct Pro	ttt Phe	gga Gly	ctg Leu 30	ctt Leu	tcc Ser	cta Leu	ttc Phe	agc Ser 35	cca Pro	aag Lys	ttg Leu	Gly ggg	tgg Trp 40	209
tgg Trp	gag Glu	aag Lys	agg Arg	ggt Gly 45	tgg Trp	agt Ser	gaa Glu	tcc Ser	atc Ile 50	tct Ser	att Ile	caa Gln	att Ile	cca Pro 55	gct Ala	257
Gly ggg	att Ile	act Thr	cta Leu 60	gga Gly	gtc Val	ttc Phe	ctg Leu	gct Ala 65	tgt Cys	ttt Phe	Gly ggg	ctc Leu	aaa Lys 70	ctt Leu	agc Ser	305
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cag Gln	gca Ala 90	atg Met	aat Asn	cct Pro	tct Ser	gca Ala 95	cac His	tcc Ser	tcc Ser	ccc Pro	cac His 100	att Ile	cct Pro	gac Asp	act Thr	401
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ccc		00> :		cato	ca ta	aacc	taaa <sup>.</sup>	t gad	gaata	aaat	atg	gege	ttc (	gggg	aaggag	60

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gga cag aaa ata tac ccc tca cat cat cgg a Gly Gln Lys Ile Tyr Pro Ser His His Arg I 15 20	
ata gct tca ttg aag tgt cag cac tca tcc a Ile Ala Ser Leu Lys Cys Gln His Ser Ser I 30 35	
agg aaa aat agc aac agt aca acg ggg tgg c Arg Lys Asn Ser Asn Ser Thr Thr Gly Trp L 50 55	
atg ggc ata ggg aat agc ggc tca aat gta g Met Gly Ile Gly Asn Ser Gly Ser Asn Val V 65 70	
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<211> 1476

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<220>

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<222> (111)..(488)

<400> 203

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Met Pro
1

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		5					10					12				
act o																212
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ttt ( Phe (																308
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gaa d Glu 1																404
aag ( Lys (																452
gaa a Glu <i>l</i> 115											tga *	tcca	a ta	aacca	agaa	502
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gctgttctat attacacagg tttgttgttg ttttttttaa aaaagaaatt aagcagtagt	1402
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tct ccc cct gac aca gag aag ggg cct tgg tat tta tat tta aga aat Ser Pro Pro Asp Thr Glu Lys Gly Pro Trp Tyr Leu Tyr Leu Arg Asn 80 85 90	468

gaa gat aat att aat aat gat gga agg aag act ggg ttg cag gga ctg Glu Asp Asn Ile Asn Asn Asp Gly Arg Lys Thr Gly Leu Gln Gly Leu

tgg tct ctc ctg ggg ccc ggg acc cgc ctg gtc ttt cag cca tgc tga Trp Ser Leu Leu Gly Pro Gly Thr Arg Leu Val Phe Gln Pro Cys \*

tgad	ccaca	acc o	ccgt	ccago	gc ca	agaca	accad	ccc	cca	ccc	acto	gtcgt	gg 1	tggc	cccaga	624
tct	ctgta	aat t	tttat	tgtag	ga gt	ttga	agcto	g aag	gccc	cgta	tatt	taat	tt a	attti	tgttaa	684
aca	gaaa	agt g	gcato	ccttt	cc co	ctcca	aaaa	a aaa	aaaa	a						721
	0.4		205													
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atto	cctga	acg	Met				L Ala						y Pro		c tca r Ser	109
			cct													157
Asp	GIu 15	Leu	Pro	GIY	Asp	20	Ser	Ser	Gin	GIU	25	Asp	GIU	Asp	TÀL	
gat	ttt	gaa	gat	cgg	gtc	agc	gac	tcg	ggt	tca	tat	tcc	tca	gcg	agt	205
30	Pne	GIU	Asp	Arg	35	ser	Asp	ser	GTĀ	40	IÀT	per	ser	Ala	45	
agc	gat	tat	gat Asp	gat	ctt	gag	cct	gaa	tgg	ctg	gac	agt	gtg	cag	aaa	253
ser	Asp	Tyr	Asp	50	ьeu	GIU	PIO	GIU	55	ьеи	Asp	261	vai	60	цуз	
			ctg Leu													301
ASII	GTÀ	GIU	65	Pne	ıyı	ьeu	GIU	70	per	Giu	Asp	Giu	75	GIU	DCI	
ctc	ctt	cct	gag Glu	aca	cca	act	gtg	aac	cat	gtc	agg	ttc	agt Ser	gaa	aat Asn	349
ьeu	ьеи	80	Giu	Till	PIO	1111	85	ASII	1115	vai	Arg	90	DCI	GIU	71511	
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GIU	95	тте	11e	GIU	Asp	100	IÄT	гур	Giu	Arg	105	цуз	TYL	Giu	110	
			cag													445
110	ьeu	гу	Gln	FIIE	115	пЛя	116	neu	AT G	120	пур	Arg	пси	ьçu	125	
			aat Asn													493
гув	Arg	Cys	ASII	130	пуs	ASII	Ser	VOII	135	VOII	G±y	110	vul	140	110	

cta Leu	aag Lys	cat His	cag Gln 145	tcc Ser	aat Asn	cag Gln	aag Lys	aca Thr 150	gga Gly	gtc Val	att Ile	gtc Val	caa Gln 155	cag Gln	cgg Arg	541
tac Tyr	aaa Lys	gat Asp 160	gtg Val	aat Asn	gtt Val	tat Tyr	gta Val 165	aac Asn	ccc Pro	aaa Lys	aag Lys	cta Leu 170	act Thr	gtt Val	atc Ile	589
aaa Lys	gcc Ala 175	aaa Lys	gag Glu	cag Gln	ctc Leu	aag Lys 180	ctt Leu	ctg Leu	gaa Glu	gtg Val	ctg Leu 185	gtt Val	gga Gly	att Ile	att Ile	637
cat His 190	cag Gln	acc Thr	aag Lys	tgg Trp	agc Ser 195	tgg Trp	aga Arg	aga Arg	acc Thr	gga Gly 200	aag Lys	cag Gln	ggt Gly	gat Asp	gga Gly 205	685
gag Glu	agg Arg	ctt Leu	gtg Val	gtt Val 210	cat His	ggc Gly	ctg Leu	ctg Leu	cca Pro 215	GJA aaa	gga Gly	tct Ser	gct Ala	atg Met 220	aag Lys	733
agc Ser	ggt Gly	cag Gln	gta Val 225	ctc Leu	att Ile	ggt Gly	gat Asp	gtc Val 230	ctt Leu	gtt Val	gct Ala	gtg Val	aat Asn 235	gat Asp	gtc Val	781
gat Asp	gtt Val	act Thr 240	act Thr	gaa Glu	aac Asn	atc Ile	gag Glu 245	aga Arg	gtt Val	ctg Leu	tct Ser	tgc Cys 250	att Ile	cct Pro	gga Gly	829
						aca Thr 260										877
						cag Gln										925
tta Leu	gtc Val	aag Lys	ctt Leu	ctc Leu 290	tgg Trp	gga Gly	gaa Glu	gag Glu	gtt Val 295	gaa Glu	ggt Gly	atc Ile	cag Gln	cag Gln 300	agt Ser	973
						atc Ile										1021
						gag Glu										1069
						ctt Leu 340										1117
ctc Leu	tgt					aac										1165

					Gly										gaa Glu	1213
				Leu	cta Leu										ctt Leu	1261
			Arg		atg Met											1309
					gat Asp											1357
					ttt Phe 435											1405
					agc Ser											1453
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					aag Lys											1549
					gca Ala											1597
					ttg Leu 515											1645
					ccc Pro											1693
					ctg Leu											1741
	Leu				aga Arg											1789
					act Thr					Glu						1837
ttt	ttg	cta	gtt	gtt	ggc	ttg	aaa	cat	tat	atg	cta	tgt	gta	cta	tta	1885

Phe 590	Leu	Leu	Val	Val	Gly 595	Leu	Lys	His	Tyr	Met 600	Leu	Сув	Val	Leu	Leu 605	
								gct Ala								1933
-	-			_		_		aca Thr 630								1981
_	_		_		_	-		cta Leu	_				_		_	2029
_		_	-	-				act Thr								2077
								agt Ser								2125
_	_					_	_	aga Arg								2173
								tcc Ser 710								2221
		_	_			_	_	gat Asp			_					2269
_	-	-	_		_		_	gaa Glu		_			_			2317
_	_	-			-			gtc Val			-					2365
								ttg Leu		_	-					2413
								aaa Lys 790								2461
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				_			_	cag Gln		-						2557

	815					820					825					
			aag Lys													2605
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			gtg Val													2749
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caga	atto	ıct g	gaaat	caat	a ca	acaaa	ıgaga	a taa	agtt	tag	ctto	tttt	ta c	ctatt	caata	3009
ttga	acat	aa t	tatto	gttaa	ıa ta	attga	gato	g aaa	tgct	gtt	ggat	ttga	ata d	catta	aatct	3069
taat	gtaa	ıta t	tgta	agac	t tt	tgag	gaata	a tac	ttga	atta	aaat	gtga	aa ç	gaagg	gattg	3129

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3189

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<sup>&</sup>lt;211> 3186

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (71)..(2836)

<sup>&</sup>lt;400> 206

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attcctgacg				cg cgt ccg ago er Arg Pro Sei 10	
gac gag ctc Asp Glu Leu 15	cct gga gac Pro Gly Asp	ccc tct tca Pro Ser Ser 20	caa gaa gaa Gln Glu Glu 25	a gat gag gac u Asp Glu Asp 5	tat 157 Tyr
				t tcc tca gcg r Ser Ser Ala	
agc gat tat Ser Asp Tyr	gat gat ctt Asp Asp Leu 50	gag cct gaa Glu Pro Glu	tgg ctg gac Trp Leu Asr 55	c agt gtg cag p Ser Val Gln 60	aaa 253 Lys
				t gaa gaa gaa p Glu Glu Glu 75	
ctc ctt cct Leu Leu Pro 80	gag aca cca Glu Thr Pro	act gtg aac Thr Val Asn 85	cat gtc agg His Val Arg	g ttc agt gaa g Phe Ser Glu 90	aat 349 Asn
				a aag tat gaa s Lys Tyr Glu 5	
aaa ctc aag Lys Leu Lys 110	cag ttt acc Gln Phe Thr 115	Lys Ile Leu	aga agg aaa Arg Arg Lys 120	a aga ctt tta s Arg Leu Leu	ccc 445 Pro 125
				a cca gta tcc y Pro Val Ser 140	
cta aag cat Leu Lys His	cag tcc aat Gln Ser Asn 145	cag aag aca Gln Lys Thr 150	Gly Val Ile	t gtc caa cag e Val Gln Gln 155	cgg 541 Arg
tac aaa gat Tyr Lys Asp 160	Val Asn Val	tat gta aac Tyr Val Asn 165	ccc aaa aag Pro Lys Lys	g cta act gtt s Leu Thr Val 170	atc 589 Ile
aaa gcc aaa Lys Ala Lys 175	gag cag ctc Glu Gln Leu	aag ctt ctg Lys Leu Leu 180	gaa gtg ctg Glu Val Leu 185	g gtt gga att u Val Gly Ile 5	att 637 Ile
cat cag acc His Gln Thr 190	aag tgg agc Lys Trp Ser 195	Trp Arg Arg	acc gga aag Thr Gly Lys 200	g cag ggt gat s Gln Gly Asp	gga 685 Gly 205
gag agg ctt Glu Arg Leu	gtg gtt cat Val Val His 210	ggc ctg ctg Gly Leu Leu	cca ggg gga Pro Gly Gly 215	a tct gct atg y Ser Ala Met 220	aag 733 Lys

		att Ile						781
		aac Asn						829
		ctg Leu						877
		aga Arg 275						925
		tgg Trp						973
		cat His						1021
		gaa Glu						1069
		aaa Lys						1117
		gaa Glu 355						1165
 		gga Gly			 -		_	1213
		cta Leu						1261
		atg Met						1309
		gat Asp						1357
		ttt Phe 435						1405

	aaa Lys	-			_	-	_		_	-	_	_		_	_	1453
	agt Ser															1501
	cca Pro	_	-		_	_	_		-	_	_		_	_	_	1549
	gct Ala 495	-	_		_	_	_					_	_		-	1597
	aag Lys	-	_			_		-	_		-	-			•	1645
_	ctg Leu			_	_			-			_	_				1693
_	gaa Glu				_				-		_	_	-		-	1741
	gaa Glu															1789
	ttg Leu 575				_		-	-			_	_			-	1837
_	tcc Ser		_			_				_	_	-			_	1885
	gtc Val															1933
_	gaa Glu			-				-		_	_		-	-	_	1981
	ttc Phe					_	_			_	_	_			_	2029
	att Ile 655		_								-	_				2077
aca	tgc	aga	aga	acg	ctt	ttt	ggt	gac	tat	tcc	tta	aag	aca	cgc	aag	2125

Thr 670	Cys	Arg	Arg	Thr	Leu 675	Phe	Gly	Asp	Tyr	Ser 680	Leu	Lys	Thr	Arg	Lys 685		
	_													gaa Glu 700		21	L73
														gta Val		22	221
-		-	_		-			-			-	_	-	ggg Gly		22	269
_		_	-			_	_							ttt Phe	_	23	317
														ata Ile		23	365
														cac His 780		24	113
_	-		_				-							ctt Leu		24	161
	-													aag Lys		25	509
														aca Thr		25	57
														gat Asp		26	05
														gtg Val 860		26	53
	-	-							_	_				cca Pro		27	01
														aaa Lys		27	49
														gcc Ala		27	97

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cacaaagaga	taaagtttag	cttcttttta	ctattcaata	ttgaacataa tattgttaaa	2966
tattgagatg	aaatgctgtt	ggatttgata	cattaaatct	taatgtaata ttgtaagact	3026
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tatataatgt	taatttattg	actagtttga	aataatgtga	agtgtttttt atatcagatt	3146
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	g gcg															491
Ca Hi	ıc agg .s Arg	gga Gly 65	Ala	agg Arg	ctg Leu	gct Ala	gcc Ala 70	gcc Ala	tcg Ser	ctg Leu	tgg Trp	ccg Pro 75	gat Asp	gga Gly	Gly aaa	539
	g caq p Glr 8(	Gly														587
Pi	a gga o Gly	cac His	agt Ser	gag Glu	ggc Gly 100	ctg Leu	GJÀ âââ	gca Ala	gcc Ala	act Thr 105	gac Asp	gcc Ala	cat His	gcc Ala	ttc Phe 110	635
	t tat u Tyr															683
	ga atg .y Met															731
	g tgo y Cys															779
	c ccc a Pro 160	Pro														827
	it tct r Ser 5															875
aa Ly	ıg tgt rs Cys	ctc Leu	ccc Pro	acc Thr 195	agc Ser	cag Gln	gtg Val	aag Lys	acc Thr 200	act Thr	ctg Leu	aca Thr	gag Glu	gct Ala 205	cca Pro	923
	g act y Thr															971
	t cct u Pro															1019
	a cca eu Pro 240	Tyr														1067
	a gtt ir Val 55															1115

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aac agt ggg cct gca atc tta gat ccc atc ctt gcc ttc ttc gag gga Asn Ser Gly Pro Ala Ile Leu Asp Pro Ile Leu Ala Phe Phe Glu Gly 305 310 315	1259										
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ttc ctg caa acc acc ctc caa ggc ctg tcc cac acg atc aag gca ggg Phe Leu Gln Thr Thr Leu Gln Gly Leu Ser His Thr Ile Lys Ala Gly 335 340 345 350	1355										
aaa gat agg cag gag tcc cct cac gaa gtc ctc aag tcc tgg ccc ctc Lys Asp Arg Gln Glu Ser Pro His Glu Val Leu Lys Ser Trp Pro Leu 355 360 365	1403										
tgg cgc tct gga agc ggt act gta tct ctc tcc aag gcc tgg tca agc Trp Arg Ser Gly Ser Gly Thr Val Ser Leu Ser Lys Ala Trp Ser Ser 370 375 380	1451										
act aag tgc att tac aaa tct ctg aga atg ttt ttt tta tac taa aat Thr Lys Cys Ile Tyr Lys Ser Leu Arg Met Phe Phe Leu Tyr * 385 390 395	1499										
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<220>

<221> CDS

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gccgcttctc tgcccgagtt aggtttcgcc cagcgcaatt tctttctcta tgtactttgc 180
gaataagttt cggagcatcg gttaacagcc tatgggtgaa atttggcttt cattcatgaa 240

tgagaaatta ttct	tgacag aagtattt	ca aaagaaaaat	Me	g gcc tca 296 t Ala Ser 1
gca gta ctt agt Ala Val Leu Ser 5	tct gtt ccc acc Ser Val Pro Th	c acc gct tct r Thr Ala Ser	cgt ttt gcc Arg Phe Ala 15	ctg tta 344 Leu Leu
caa gtg gat agt Gln Val Asp Ser 20	ggc agt ggc tc Gly Ser Gly Ser 25	t gat tct gaa r Asp Ser Glu 30	cct gga aaa Pro Gly Lys	ggt aaa 392 Gly Lys 35
	gga aag tot caa Gly Lys Ser Gli 40			
	aga gag aaa aga Arg Glu Lys Arg			
	gag ctc agg aat Glu Leu Arg Ass 7	n Leu Ala Phe		
aaa tcc tcc cat Lys Ser Ser His 85	gct gtt tgt aad Ala Val Cys Asi 90	c gct caa cat n Ala Gln His	gat ctt cca Asp Leu Pro 95	ttg tca 584 Leu Ser
	aag gat tca cga Lys Asp Ser Arg 105			
caa aga gat gag Gln Arg Asp Glu	cag ctg aca tc Gln Leu Thr Se 120	t gaa atg ttt r Glu Met Phe 125	gaa gca gat Glu Ala Asp	ctt gag 680 Leu Glu 130
aag gca ttg tta Lys Ala Leu Leu 135	cta agt aaa cta Leu Ser Lys Le			
	gaa aat act to Glu Asn Thr Se 15	r Thr Gln Ser		
aaa gat aaa aga Lys Asp Lys Arg 165	aag aat cat cag Lys Asn His Gli 170	g gga aaa gac n Gly Lys Asp	aga cct ctc Arg Pro Leu 175	aca gta 824 Thr Val
	ttt cat tcg gad Phe His Ser Gla 185			
	aaa gat gga ag Lys Asp Gly Ar 200			
gaa agg aaa gat	gct gaa atc ca	g aag ctg aaa	aat gta atc	act caa 968

Glu	Arg	Lys	Asp 215	Ala	Glu	Ile	Gln	Lys 220	Leu	Lys	Asn	Val	Ile 225	Thr	Gln	
		-	_		aag Lys	_	~	_	_	_		_			_	1016
					ggt Gly				-	_	_	_			-	1064
					caa Gln 265	_		_						-		1112
				_	gca Ala				_	_					_	1160
					gcc Ala											1208
				_	cag Gln	_		tga *	ttad	a tt	agco	tttg	g aag	gtcaa	acac	1260
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aact	atgo	ag t	tttt	gttg	ga aç	gaac	taaa	ago	aact	agc	tccc	taat	gg t	ctat	aattt	1380
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acaaatacca gttcatacat tcttgttcca ataggagtt atg gga gga aaa att Met Gly Gly Lys Ile
1 5

att cca agc aat cac aca gga tca act ttt tct cct tgt aga ata tgt 222

Ile Pro Se	r Asn His 10	Thr Gly	Ser Th	r Phe 15	Ser	Pro	Cys .	Arg	Ile 20	Cys	
gtc atc ac Val Ile Th		-	His Pr								270
att aaa ag Ile Lys Se 4	r Ile Ser	_	_	•		_	-	_		_	318
aac aag gt Asn Lys Va 55			Lys Ar								366
att atc ta Ile Ile Ty 70					taa * 80	tgac	agat	cca	aatga	, lacc	417
ttagaatcca	gtagcata	g cttag	catac t	tctcta	gca	gttt	gagg	tg c	ctaat	tttag	477
gtatactttc	acctaaaga	aa attct	cagct c	ccccaa	att	aggt	atct	ca ç	gagg	tgtag	537
tatctgttat	attaggtto	ct gtgct	actat c	cctata	atg	ссса	.ggat	gg a	aggag	gggga	597
aggcaggcct	ttgaaagga	ng aactc	taata g	caatat	aac	aaga	tatti	tt g	gtccc	ttcta	657
gttgtattaa	actagtato	jt cgagt	tctgt a	aaattt	agg	tgac	taacı	tc t	tctt	tacca	717
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aggtacttat	gggcaccto	a ccata	taaaa c	cgataa	aag	cata	cctct	t c	tggt	taagg	240
tggggaggat	cctcgagct	c cctga	attgt c	ctttta	ccc	tgtc	tcccc	c t	cccc	cttgt	300
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100

95

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_			_	gtg Val							717
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				gaa Glu							1005

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Glu Ala Leu Ser Ala Arg Ile Pro Leu Gln Arg Ala Leu Pro Glu Val

165

170

175

480

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Arg His Pro Leu Cys Leu Gln Gln His Pro Gln Asp Ser Leu Pro Thr

180 185 190

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280
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Ser Arg Val Val Ser Pro Val Ile Asp Val Ile Asp Trp Lys Thr Phe

305

310

315

320

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325

330

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355

360

365

478

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		-		agg Arg	_			_				1536
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							ccg Pro								2916
							gac Asp								2964
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Ser	aag Lys 1360				Ala					Ala						4308
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<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Homo sapiens

<sup>&</sup>lt;220>

<sup>&</sup>lt;221> CDS

<sup>&</sup>lt;222> (371)..(595)

<sup>&</sup>lt;400> 221

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agt gtc agc tat ggc cat gtg gcc gcc tgc cag cta atg ggc ccc cac Ser Val Ser Tyr Gly His Val Ala Ala Cys Gln Leu Met Gly Pro His 15 20 25	457
acc ctg gcc ttg agg gtg gga gag agc cag ctc ctc ctg cag agc ccc Thr Leu Ala Leu Arg Val Gly Glu Ser Gln Leu Leu Gln Ser Pro 30 35 40 45	505
cag gtg agt gag aag agg agt tgt ggg agg a	553
tgt cag gaa gca ttt aca gaa cac caa acc tgg gcc agg tag agctcta Cys Gln Glu Ala Phe Thr Glu His Gln Thr Trp Ala Arg * 65 70 75	602
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1 5 10

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cag act gag ggc ggc ttc cag aag ggg agg ggc cgg gac agc gag agc Gln Thr Glu Gly Gly Phe Gln Lys Gly Arg Gly Arg Asp Ser Glu Ser 50 55 60	251
tgg gcc tac cct gtg gcc ccc atg ttc agc cct cct tcc tca gag cct Trp Ala Tyr Pro Val Ala Pro Met Phe Ser Pro Pro Ser Ser Glu Pro 65 70 75	299
cac ctg ggc ctc ctg atg gct cct gtc ccc tgc ctg ccc tgc tgt acg His Leu Gly Leu Leu Met Ala Pro Val Pro Cys Leu Pro Cys Cys Thr 80 85 90	347
cct gcc cac cct tgg cct gtg tgc tcc gat aag cca ttg ctg tgt tca Pro Ala His Pro Trp Pro Val Cys Ser Asp Lys Pro Leu Leu Cys Ser 95 100 105 110	395
ctg ggc cag tcg gtg gtg gag ccc tcc taa g gattcacggt ggcccgcct Leu Gly Gln Ser Val Val Glu Pro Ser * 115 120	446
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tgg gaa tct ata tat gtg aca cag gaa tta cct ctg aag cag ttc atg Trp Glu Ser Ile Tyr Val Thr Gln Glu Leu Pro Leu Lys Gln Phe Met 15 20 25	157									
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tcc act ttt gaa gaa aat tgg aaa tgg gaa gac ctt ttt gag aag cag Ser Thr Phe Glu Glu Asn Trp Lys Trp Glu Asp Leu Phe Glu Lys Gln 45 50 55 60	253									
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ttc acc cat agc tca tcc ctt act gtt cat ttt aga att cat act ggt Phe Thr His Ser Ser Ser Leu Thr Val His Phe Arg Ile His Thr Gly 145 150 155	541									
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			_				_							ctc Leu		637
														ctt Leu		685
_								-						aag Lys		733
-	_		_		_	_		-			_	_		cag Gln 235	_	781
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	_	_		-										act Thr		877
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